

RESULT 15

JC5059
bitiscetin beta chain - puff adder
C/Species: Bitis arietans (puff adder)
C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 12-Feb-1999
C/Accession: JC5059; JC5917
R/Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz
submitted to JIPID, January 1997.
A/Description: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor
A/Reference number: JC5058
A/Accession: JC5059
A/Molecule type: protein
A/Residues: 1-125 <MAT>
A/Experimental source: snake venom
R/Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz
Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997
A/Title: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor modul
A/Reference number: JC5916

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:36:04 ; Search time 8 Seconds
(without alignments)
1223.649 Million cell updates/sec

Title: US-09-811-367B-3
Perfect score: 1029
Sequence: 1 MADSSIVSTLELPEAPQVQD.....GLQASCEVALQWICKVKVLY 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 40997

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180.5	17.5	179	1	Q9mk9 macaca mula
2	178.5	17.3	179	1	Q13241 homo sapien
3	178.5	17.3	179	1	Q9mz41 pan troglod
4	152.5	14.8	146	1	IXB_TRIPL
5	150.5	14.6	148	1	CVXB_CRODU
6	146.5	14.2	163	1	V2339 FOWPV
7	145	14.1	146	1	MMHB_AGRHA
8	144	14.0	149	1	CLE2_HUMAN
9	139	13.5	157	1	MMHA_AGRHA
10	138	13.4	167	1	V008_FOWPV
11	125.5	12.2	133	1	RHCA_AGRKH
12	124.5	12.1	117	1	CHBB_CROHO
13	124.5	12.1	123	1	ABAA_TRIAB
14	120.5	11.7	158	1	CVXA_CRODU
15	119	11.6	133	1	BOTB_BOTJA
16	113.5	11.0	125	1	BOTB_BOTJA
17	110.5	10.7	155	1	PLC_HALLA
18	109.5	10.6	129	1	RHCB_AGRKH
19	108.5	10.5	125	1	ABAB_TRIAB
20	105	10.2	174	1	PAP3_MOUSE
21	104	10.1	152	1	IXA_TRIPL
22	103	10.0	175	1	PAP1_MOUSE
23	103	10.0	175	1	PAP2_MOUSE
24	102.5	10.0	162	1	LECB_MEGRO
25	101.5	9.9	123	1	ECHB_ECHCA
26	101.5	9.9	158	1	LECG_TRIST
27	101	9.8	175	1	PAP1_HUMAN
28	97.5	9.5	165	1	LITH_RAT
29	97	9.4	127	1	CHBA_CROHO
30	97	9.4	134	1	ABAA_TRIAB
31	97	9.4	135	1	LECG_CROAT
32	95	9.2	174	1	PAP3_RAT
33	94	9.1	175	1	PAP1_RAT

34	93.5	9.1	118	1	ABBB_TRIAB	P81116 trimeresuru
35	93	9.0	158	1	NKGF_PANTR	Q95mil pan troglod
36	93	9.0	163	1	ANP_HEMAN	P05140 hemitripten
37	92	8.9	158	1	NKGF_HUMAN	O43908 homo sapien
38	91	8.8	175	1	PBCG_MESAU	Q92778 mesocricetu
39	90	8.7	166	1	LITA_HUMAN	P05451 homo sapien
40	89.5	8.7	166	1	LITB_HUMAN	P48304 homo sapien
41	86.5	8.4	133	1	ECHA_ECHCA	P81017 echis carin
42	86	8.4	135	1	LECG_BITAR	Q9psn0 bitis carin
43	86	8.4	135	1	LECG_LACST	Q9psm4 lachesis st
44	86	8.4	175	1	LITH_BOVIN	P23132 bos taurus
45	85.5	8.3	132	1	ABBA_TRIAB	P81115 trimeresuru

ALIGNMENTS

RESULT 1

CD94_MACMU

ID_CD94_MACMU STANDARD; Q9MK7; Q9MKX8; PRT; 179 AA.

AC Q9MKX8; Q9GK91; Q9MK7; Q9MKX8;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell

DE lectin-like receptor subfamily D, member 1).

GN KURDI OR CD94.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheidae; Macaca.

OX NCBI_TaxID=9544;

XP [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RX MEDLINE=20322487; PubMed=10866118;

RA LaBonte M.L., Levy D.B., Letvin N.L.;

RT "Characterization of rhesus monkey CD94/NKG2 family members and

RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,

RT and D.";

RL Immunogenetics 51:496-499(2000).

[2]

SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=21158386; PubMed=11261935;

RX Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;

RT "Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative

RT splicing of 5' exons in rhesus monkey decidua.";

RL Immunogenetics 53:69-73(2001).

CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC

CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.

CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family

CC members.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1; Synonyms=CD94-A;

CC IsoId=Q9MKX9-1; Sequence=Displayed;

CC Name=2; Synonyms=CD94-B;

CC IsoId=Q9MKX9-2; Sequence=VSP_003055;

CC Name=3; Synonyms=CD94 alt;

CC IsoId=Q9MKX9-3; Sequence=VSP_003054;

CC -!- TISSUE SPECIFICITY: Natural killer cells.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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EMBL; AF190931; AAF74527.1; -.

EMBL; AF190932; AAF74528.1; -.


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DR Genew: HGNC:6378; KLRD1.
DR MM: 602894; -.
DR GO: GO:0005886; C:plasma membrane; TAS.
DR GO: GO:0004888; F:transmembrane receptor activity; TAS.
DR GO: GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE: PS50041; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; 3D-structure.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 34 MAVFKTLWLRLISGTLGIICLSMATLGLLKNS -> MAA
(in isoform 3).
FT VARSPLIC 105 105 /FTid=VSP_003052.
FT VARSPLIC 105 105 /FTid=VSP_003053.
FT SEQUENCE 179 AA; 20497 MW; 1884D99E8D9583A7 CRC64;
Query Match 17.3%; Score 178.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. No. 9.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
Qy 44 GLLTIVLMSLLMYQRIILCCGS-----KDSCTCHPCSPILWTRNGS 84
Db 14 GTLGIICLSMATLGIILKNSFTKLSIEPTPGPNIELQKSDC--C-SQCKWVGRC 70
Qy 85 HCYVFSMEKDWNSLKFADKSHLLTFPDNQVKLFGEVIGDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNEHRLCASQKSLQLQNTDELDFMSS--SQQFYWIGLSYEHTAW 128
Qy 142 RWEGGPALSRILTN---SLIQRCGAIHRNG-LQASCEVALQWICKVL 187
Db 129 LWENGSAISQYLPFPFTEFTKNCIAYNPNGNALDESCDKNRVICKQOL 178
RESULT 3
CD94_PANTR STANDARD; PRT; 179 AA.
AC Q9M241;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1).
GN KLRD1 OR CD94.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20350666; PubMed=10894168;
RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
RA Muir D.G., Canavez F., Cooper S.L., Valliant N.M., Lanier L.L.,
RA Parham P.;
RA "Rapid evolution of NK cell receptor systems demonstrated by
RT comparison of chimpanzees and humans.";
RL Immunity 12:687-698(2000).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=21623889; PubMed=11751968;
RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guechtein L.A., Uhrberg M., Parham P.;
RT "Conservation and variation in human and common chimpanzee CD94 and
RT NKG2 genes.";
RL J. Immunol. 168:240-252(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q9M241-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q9M241-2; Sequence=VSP_003056;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF259054; AAF86964.1; -.
DR HSP: P22897; IREG.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE: PS50041; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 105 105 /FTid=VSP_003056.
FT SEQUENCE 179 AA; 20493 MW; 724D99E8D9587E7 CRC64;
Query Match 17.3%; Score 178.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. No. 9.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
Qy 44 GLLTIVLMSLLMYQRIILCCGS-----KDSCTCHPCSPILWTRNGS 84
Db 14 GTLGIICLSMATLGIILKNSFTKLSIEPTPGPNIELQKSDC--C-SQCKWVGRC 70
Qy 85 HCYVFSMEKDWNSLKFADKSHLLTFPDNQVKLFGEVIGDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNEHRLCASQKSLQLQNTDELDFMSS--SQQFYWIGLSYEHTAW 128
Qy 142 RWEGGPALSRILTNLI---QRCGAIHRNG-LQASCEVALQWICKVL 187
Db 129 LWENGSAISQYLPFPFTEFTKNCIAYNPNGNALDESCDKNRVICKQOL 178
RESULT 4
IXB_TRIFL
ID -IXB TRIFL STANDARD; PRT; 146 AA.
AC P23807; O91247;
DT 01-NOV-1991 (Rel. 20, Created)

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DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PRO1504; PNCREATITSP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Lectin; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 148 CONULXIN BETA.
FT DOMAIN 34 145 C-TYPE LECTIN.
FT DISULFID 26 26 INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
(POTENTIAL).
FT DISULFID 27 38 BY SIMILARITY.
FT DISULFID 55 144 BY SIMILARITY.
FT DISULFID 100 100 INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
(POTENTIAL).
FT DISULFID 121 136 BY SIMILARITY.
SQ SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;

Query Match 14.6%; Score 150.5; DB 1; Length 148;
Best Local Similarity 31.4%; Pred. No. 4.9e-08;
Matches 38; Conservative 18; Mismatches 42; Indels 23; Gaps 6;

QY 35 LSRFAMVALGLLTILVMSLLMYQRIILCGSKDSTCSHCPSCLILWTRNGSHCYFYSMEKK 94
Db 1 MGRFIFVSGLL-VVFLSL-----SGSEAGFC-----CPSHWSSYDRYCYKVFQEM 46
QY 95 DWSSSLKFCADK--GSHLLTFPDNQ-----VKLFGEYLQDFYWIGLRNI---DGWRWEG 145
Db 47 TWADAERFCTQQTGSHLVSHFSTEEVDVVMKTHQSLKSTFFWIGANNIWNKCNQWSD 106

QY 146 G 146
Db 107 G 107

RESULT 6
V239_FOWPV STANDARD; PRT; 163 AA.
ID V239_FOWPV STANDARD; PRT; 163 AA.
AC P14371; Q9J500;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative C-type lectin protein FPV239 (BamHI-ORF8).
GN FPV239.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
RN [2]
RP SEQUENCE OF 1-116 FROM N.A.
RC STRAIN=FP-9 / Isolate HP-438;
RX MEDLINE=8829622; PubMed=2836548;
RA Tomley F., Binns M., Campbell J., Boursnell M.E.G.;
RT "Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
of fowlpox virus.";
RL J. Gen. Virol. 69:1025-1040(1988).
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC EMBL; AF198100; AAF44583.1; -.
DR
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DR EMBL; D00295; BAA00203.1; -.
DR PIR; H29963; WMVZB8.
DR HSP; P05140; ZAFP.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Hypothetical protein; lectin.
FT DOMAIN 48 159 C-TYPE LECTIN.
SQ SEQUENCE 163 AA; 18635 MW; 5156DC892885532 CRC64;

Query Match 14.2%; Score 146.5; DB 1; Length 163;
Best Local Similarity 26.8%; Pred. No. 1.4e-07;
Matches 33; Conservative 24; Mismatches 57; Indels 9; Gaps 3;

QY 73 PSCPILWTRNG-----SHCYFYSMEKKDWNSLSLKFCADKSHLLTFPDNQGVKLFGEYL 127
Db 41 PDIKILYCKEGWGVYKNKYFFSEKNNKSLAVERCKMDGHLTSSKEEFKILRYKG 100
QY 128 QDPYTWGLRNI--QWRWEGGPAISRLITNSLIORCGAIHRNGLOASCEVALQWICK 184
Db 101 PGNHWIGIEKVDENGTWKLKEDGSSYD-NIVPIKIGDCAVLSDRSINSFCLPKKWICR 159
QY 185 KVL 187
Db 160 IIL 162

RESULT 7
MMHB_AKGHA STANDARD; PRT; 146 AA.
ID MMHB_AKGHA STANDARD; PRT; 146 AA.
AC Q9Y192;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mamushigin beta chain precursor.
OS Agkistrodon halsi blomhoffi (Mamushi) (Gloydus blomhoffii).
OC Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Gloydus.
OX NCBI_TaxID=242054;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 24-56, SUBUNIT, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=98319530; PubMed=9657448;
RA Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M.,
RA Suzuki M., Matsui T., Titani K., Yoshioka A.;
RT "The cDNA cloning and molecular characterization of a snake venom
platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon
halsi blomhoffii venom.";
RL Thromb. Haemost. 79:1199-1207(1998).
CC -!- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet
aggregation at low-shear stress. At high-shear stress, aggregation
is inhibited.
CC -!- SUBUNIT: Heterodimer of alpha and beta chains; disulfide-
linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=15413; METHOD=Electrospray;
RANGE=24-146.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC EMBL; AB019616; BAA34425.1; -.
DR HSP; P23807; IIXX.
DR GO; GO:0005576; C:extracellular; IC.
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GO: GO:0007596; P:blood coagulation; IDA.
 DR InterPro: IPR001304; LECTIN_C.
 DR Pfam: PF00059; LECTIN_C_1.
 DR SMART: SM00034; CLECT_1.
 DR PROSITE: PS00615; C-TYPE LECTIN 1; 1.
 DR PROSITE: PS00411; C-TYPE LECTIN 2; 1.
 KW Blood coagulation; LECTIN; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 146 MAMUSHIGIN BETA CHAIN.
 FT DOMAIN 32 143 C-TYPE LECTIN.
 FT DISULFID 25 36 BY SIMILARITY.
 FT DISULFID 53 142 BY SIMILARITY.
 FT DISULFID 98 98 INTERCHAIN (WITH C-103 IN ALPHA CHAIN)
 FT DISULFID 119 134 (BY SIMILARITY).
 FT DISULFID 134 (BY SIMILARITY).
 FT SEQUENCE 146 AA; 17064 MW; 9EDA84BDC24E76D CRC64;
 Query Match 14.1%; Score 145; DB 1; Length 146;
 Best Local Similarity 27.3%; Pred. No. 1.7e-07;
 Matches 45; Conservative 17; Mismatches 55; Indels 48; Gaps 8;
 QY 35 LSRFAMVALGLLTVILMSILMYQRIILCCGSKDSTCHSPILWTRNGSHCHYFSMEKK 94
 DB 1 MGRFIFLFGLLVVFV-----SLSGTGADCPSD---WSSVEGHCYRVFQKEM 44
 QY 95 DNWSLKFCD--KGSHLLTFPDNQG---VKLFGYLGQDFYWGILGRNIDGW-----RW 143
 DB 45 TWEDAEEKCTQQRKESHLVFSHSSEVDVFMVMTWPKLYDFVWGLANNI--WNECMVEM 102
 QY 144 EGGPALSRLILNSLIQRCAGHNRGLQASCEVAL-----QWICK 184
 DB 103 TDGTRLS-----HNAWITESECIAAKTTDNQWLSR 132
 RESULT 8
 CLE2_HUMAN
 ID CLE2_HUMAN STANDARD; PRT; 149 AA.
 AC Q92478; Q9BSV4; Q9UQB4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE C-type lectin superfamily member 2 (Activation-induced C-type lectin).
 GN CLECSF2 OR AICL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97190245; PubMed=9038101;
 RA Hamann J., Montgomery K.T., Lau S., Kuchelapati R., van Lier R.A.W.,
 RT "AICL, a new activation induced antigen encoded by the human NK gene
 RT complex."
 RL Immunogenetics 45:295-300 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97173880; PubMed=10072769;
 RA Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.;
 RT "Selection of cDNAs encoding putative type II membrane proteins on the
 RT cell surface from a human full-length cDNA bank."
 RL Gene 228:161-167 (1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Urinary bladder;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Expressed preferentially in lymphoid tissues,
 CC and in most hematopoietic cell types.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 DR EMBL; X96719; CAA65480.1; -;
 DR EMBL; AB015628; BAA76495.1; -;
 DR EMBL; BC005254; AAO05254.1; -;
 DR GenBank; HGNC:2053; CLECSF2.
 DR MIM; 603242; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005530; F:lectin; TAS.
 DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
 DR InterPro: IPR001304; LECTIN_C.
 DR Pfam; PF00059; LECTIN_C; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
 DR PROSITE; PS00411; C-TYPE LECTIN 2; 1.
 KW Glycoprotein; Transmembrane; LECTIN; Signal-anchor.
 FT DOMAIN 1 7
 FT TRANSMEM 8 25
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT C-TYPE LECTIN.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 79 79 M -> T (IN REF. 3).
 FT CONFLICT 107 107 D -> H (IN REF. 1).
 SQ SEQUENCE 149 AA; 17307 MW; 0B4FED23424F6C55 CRC64;
 Query Match 14.0%; Score 144; DB 1; Length 149;
 Best Local Similarity 26.5%; Pred. No. 2.2e-07;
 Matches 43; Conservative 28; Mismatches 67; Indels 24; Gaps 7;
 QY 34 HLSRFAMVALGLLTVILMSILMYQRIILCCGSKDSTCHSPILWTRNGSHCHYFSMEK 93
 DB 5 HKKCFIIVGV-LITNTIITLVKL-----TRDSQ-----SLCPYDWIGFQNKCYFSKEE 53
 QY 94 KDNWSLKFCDKSHLLTFPDNQGKLVFGYLGQDFYWGIL---RNLDGWRWEGGPALS 150
 DB 54 GDNWSKYNKSTQHADLTIDNIEEMNPLRYKCSSDHWIGLWAKNRTG-QWVDGAT-- 110
 QY 151 LRILTNLSLIQR---CGAIHNRGLQASCEVALQWICKVLY 188
 DB 111 ---FTKSGFMGRSGCGAYLSDGGAATACATCYTERKWKCRKH 149
 RESULT 9
 MHA_AGHA


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RHCA_AGRKH
ID RHCA_AGRKH STANDARD; PRT; 133 AA.
AC P81397;
DT 15-JUL-1998 (Rel. 36, Last Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Rhodocetin alpha subunit.
OS Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Calloselasma.
OX NCBI_TaxID=8717;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96420502; PubMed=8823201;
RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
RA Smith A.I., Lopez J.A., Berndt M.C.;
RT "Binding of a novel 50-kilodalton albosaggregin from Trimeresurus
RT albolaris and related viper venom proteins to the platelet membrane
RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and
RT glycoprotein Ib-mediated platelet activation.";
RL Biochemistry 35:12629-12639(1996).
CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system, inhibits vWF
CC binding, and stimulates agglutination.
CC -!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR InterPro; IPR002353; AntifreezeII.
DR Pfam; PF00059; Lectin C; 1.
DR PRINTS; PRO0356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN 9 116 C-TYPE LECTIN.
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 115 BY SIMILARITY.
FT DISULFID 92 92 INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
(POTENTIAL).
FT DISULFID 95 107 BY SIMILARITY.
SQ SEQUENCE 117 AA; 13888 MW; 07835B8C61E9EAD CRC64;

Query Match 12.1%; Score 124.5; DB 1; Length 117;
Best Local Similarity 25.8%; Pred. No. 1.5e-05;
Matches 31; Conservative 23; Mismatches 51; Indels 15; Gaps 6;

QY 75 CPILWTRNGSHCYFMSMEKKNWSLKFCAK--GSHLLTFPDNQGVKLFGEYLQDFY 132
Db 2 CPDWSSTKSYCYRPFKEKKTWEAEAREFCTQKEAHLVSM--ENRLEAVFDVMTWENNFE 61
QY 133 IGLRNIDGW-----RWEGGPALSLRILT--NSLIQRCGAIHRNGLQASSCEVALQWTC 184
Db 62 MGRDRI--WNERLLQWSDGTQVNYKAWSAEPCIV--CRATDQWL-STSCSKTHNVVCK 116

RESULT 13
ABA4_TRIAB
ID ABA4_TRIAB STANDARD; PRT; 123 AA.
AC P81114;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Albosaggregin A subunit 4.
OS Trimeresurus albobaris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Albosaggregins A and B. Structure and interaction with human
RT platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC agglutination.
CC -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
CC disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

```


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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:39:05 ; Search time 32 Seconds

(without alignments)
1853.669 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSYITLPEAPQVQD.....GLQASCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 396094

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1029	100.0	188	11	O88713	O88713 mus musculus
2	838	81.4	188	11	Q64335	Q64335 rattus norv
3	180	17.5	179	11	O54708	O54708 mus musculus
4	180	17.5	179	11	O54707	O54707 mus musculus
5	177.5	17.2	179	6	Q8MHV8	Q8MHV8 pongo pygma
6	174.5	17.0	179	6	Q8MJL3	Q8MJL3 pongo pygma
7	174.5	17.0	179	6	Q8MHY9	Q8MHY9 pongo pygma
8	171.5	16.7	179	6	Q8MJL4	Q8MJL4 pongo pygma
9	171.5	16.7	181	4	Q9NZS1	Q9NZS1 homo sapien
10	169	16.4	159	6	Q8SPX0	Q8SPX0 sus scrofa
11	168	16.3	165	11	Q9R007	Q9R007 mus musculus
12	163.5	15.9	146	13	Q9TAM0	Q9TAM0 agkistrodon
13	163.5	15.9	146	13	Q8JLW1	Q8JLW1 agkistrodon
14	163	15.8	161	6	Q95JG4	Q95JG4 bos taurus
15	161	15.6	165	6	Q9GLF4	Q9GLF4 sus scrofa
16	159.5	15.5	132	11	Q8R4K5	Q8R4K5 rattus norv

Q8BL24 mus musculus
Q8AYA4 agkistrodon
Q9GK90 macaca mla
Q8AY98 trimeresuru
Q35778 rattus norv
Q9GLF3 sus scrofa
Q8JGT6 trimeresuru
Q8WUP7 homo sapien
Q9I840 agkistrodon
Q7E045 vipera lebe
Q9MZJ6 macaca mla
Q8MHY4 pongo pygma
Q8HJ37 homo sapien
Q9DG31 agkistrodon
Q8UVC7 agkistrodon
Q9NY25 homo sapien
Q8AYA3 agkistrodon
Q9DEAL agkistrodon
Q9VGN4 agkistrodon
Q8MJH4 pongo pygma
Q9IZW9 mus musculus
Q95J54 pan troglod
Q8JIV7 agkistrodon
Q9UKQ0 homo sapien
Q8UVC6 agkistrodon
Q8AYA5 agkistrodon
Q9DEF8 agkistrodon
Q8CJ86 mus musculus

ALIGNMENTS

RESULT 1

O88713 ID O88713 PRELIMINARY; PRT; 188 AA.
AC O88713;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-AUG-1999 (TREMblrel. 11, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor Gl).
DE like receptor Gl).
GN KLRG1 OR MAFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=C.B-17 SCID;
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raulet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:409-441(1998).
RN [2] SEQUENCE OF 2-188 FROM N.A.
RP Blaser C.;
RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3] SEQUENCE FROM N.A.
RP STRAIN=129/SvevTAcBr; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=11220622;
RA Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor Gl gene (KLRG1), the mouse homologue of MAFA";
RL Immunogenetics 52:206-211(2001).
DR EMBL; AF097357; AAD03718.1; -
DR EMBL; AJ010751; CAA09342.1; -
DR EMBL; AF317727; AAK40082.1; -
DR MGD; MGI:1355294; Klrp1.

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DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match 100.0%; Score 1029; DB 11; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVQDSRWKLVKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRI 60
DB 1 MADSSYSTLELPEAPQVQDSRWKLVKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRI 60
QY 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTFFDNQGVK 120
DB 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTFFDNQGVN 120
QY 121 LFGYLGQDFYWGIRNIDGWRWEGGPPALSRLITNSLIQRCGAHNRNGLOASCEVALQ 180
DB 121 LFGYLGQDFYWGIRNIDGWRWEGGPPALSRLITNSLIQRCGAHNRNGLOASCEVALQ 180
QY 181 WICKKVL 187
DB 181 WICKKVL 187

RESULT 3
O54708 PRELIMINARY; PRT; 179 AA.
AC O54708;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD94.
GN KL8D1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB.17 SCID;
RX MEDLINE=98124458; PubMed=9464811;
RT Vance R.E., Tanamachi D.M., Hanke T., Raulat D.H.;
RT "Cloning of a mouse homolog of CD94 extends the family of C-type
RT lectins on murine natural killer cells.";
RL Eur. J. Immunol. 27:3236-3241(1997).
DR EMBL; AF030312; AAC28244.1; -.
DR MGD; MGI:1196275; Klrd1.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00022; EGF_1; 1.
SQ SEQUENCE 179 AA; 20809 MW; D59E1CB6G3139E45 CRC64;

Query Match 17.5%; Score 180; DB 11; Length 179;
Best Local Similarity 31.8%; Pred. No. 9.2e-11;
Matches 57; Conservative 25; Mismatches 75; Indels 22; Gaps 9;

QY 22 SRWLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIICGSKDST----CSHCPCSP 76
DB 7 TRWELMSVIFGIK-CLFLMVTLG---VLLINSFIQNIQSTPTTTFEVEQSECCVCL 62
QY 77 ILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTFFDNQGVKLFGEYLGQDFYWGIR 135
DB 63 DKWVGHCQNCYFISKEEKSWERSDFCASQNSLLQ-PQSRNELSPMNF-SQTFEWMGH 120
QY 136 ---RNTDGEWEGGPPALSRLITN-SLIQRCGAI---HRNGLOASCEVALOWICKV 186
DB 121 YSEKRN--AWLWEDGTVPKDLFFEFVIRPEHCIVYSPKSVSAESCENKRYICKKL 177

RESULT 4
O54707 PRELIMINARY; PRT; 179 AA.
AC O54707;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

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Db      14 GTLGIICLSMATLIGILLKNFTKLSIEPAFTPGPDIELQKSDC--C-SQEKWVGVC 70
QY      85 HCIFYSEKMDKWNSSLKFCADKGSLLTFPPNQGVKLFGEYLGQDFYWGIRNID---GW 141
Db      71 NCYFISSEKQKWNESRHLCSQKSSLLQLQNTDELDLFMS--SQQFYWIGLSYSEHTAW 128
QY      142 RWEGGPALSS---LRILTNLSLQRCGAHRNG-LQASCEVALQWICKVL 187
Db      129 LWENGSSLSQYLFPLFETFPNFCIAYNPNGNALDESCEDKNRYICKQOL 178

RESULT 7
Q8MHY9
ID Q8MHY9 PRELIMINARY; PRT; 179 AA.
AC Q8MHY9;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Natural killer cell receptor.
GN POPY-CD94.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470380; AAM78485.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20520 MW; 6744895FBD95CFA CRC64;

Query Match 17.0%; Score 174.5; DB 6; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.4e-10;
Matches 54; Conservative 15; Mismatches 70; Indels 31; Gaps 7;

QY      44 GLTIVILSLMYQRIILCCGS-----KSTCSHCPCSPILLWTRNGS 84
Db      14 GTLGIICLSMATLIGILLKNFTKLSIEPAFTPGPDIELQKSDC--C-SQEKWVGVC 70
QY      85 HCIFYSEKMDKWNSSLKFCADKGSLLTFPPNQGVKLFGEYLGQDFYWGIRNID---GW 141
Db      71 NCYFISSEKQKWNESRHLCSQKSSLLQLQNTDELDLFMS--SQQFYWIGLSYSEHTAW 128
QY      142 RWEGGPALSS---LRILTNLSLQRCGAHRNG-LQASCEVALQWICKVL 187
Db      129 LWENGSSLSQYLFPLFETFPNFCIAYNPNGNALDESCEDKNRYICKQOL 178

RESULT 8
Q8MJ14
ID Q8MJ14 PRELIMINARY; PRT; 179 AA.
AC Q8MJ14;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Natural killer cell receptor.
GN POPY-CD94.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470380; AAM78485.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20520 MW; 6744895FBD95CFA CRC64;

Query Match 17.0%; Score 174.5; DB 6; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.4e-10;
Matches 54; Conservative 15; Mismatches 70; Indels 31; Gaps 7;

QY      44 GLTIVILSLMYQRIILCCGS-----KSTCSHCPCSPILLWTRNGS 84
Db      14 GTLGIICLSMATLIGILLKNFTKLSIEPAFTPGPDIELQKSDC--C-SQEKWVGVC 70
QY      85 HCIFYSEKMDKWNSSLKFCADKGSLLTFPPNQGVKLFGEYLGQDFYWGIRNID---GW 141
Db      71 NCYFISSEKQKWNESRHLCSQKSSLLQLQNTDELDLFMS--SQQFYWIGLSYSEHTAW 128
QY      142 RWEGGPALSS---LRILTNLSLQRCGAHRNG-LQASCEVALQWICKVL 187
Db      129 LWENGSSLSQYLFPLFETFPNFCIAYNPNGNALDESCEDKNRYICKQOL 178

RESULT 9
Q9NZS1
ID Q9NZS1 PRELIMINARY; PRT; 181 AA.
AC Q9NZS1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Lectin-like receptor FL, splice variant 1 KLRFI-sl.
GN KLRFI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KLRFI, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
DR EMBL; AF175207; AAF37805.1; -.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CAE1E551 CRC64;

Query Match 16.7%; Score 171.5; DB 4; Length 181;

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470383; AAM78483.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20536 MW; 6744895EC6F8780 CRC64;

Query Match 16.7%; Score 171.5; DB 6; Length 179;
Best Local Similarity 31.2%; Pred. No. 7.1e-10;
Matches 53; Conservative 16; Mismatches 70; Indels 31; Gaps 7;

QY      44 GLTIVILSLMYQRIILCCGS-----KSTCSHCPCSPILLWTRNGS 84
Db      14 GTLGIICLSMATLIGILLKNFTKLSIEPAFTPGPDIELQKSDC--C-SQEKWVGVC 70
QY      85 HCIFYSEKMDKWNSSLKFCADKGSLLTFPPNQGVKLFGEYLGQDFYWGIRNID---GW 141
Db      71 NCYFISSEKQKWNESRHLCSQKSSLLQLQNTDELDLFMS--SQQFYWIGLSYSEHTAW 128
QY      142 RWEGGPALSS---LRILTNLSLQRCGAHRNG-LQASCEVALQWICKVL 187
Db      129 LWENGSSLSQYLFPLFETFPNFCIAYNPNGNALDESCEDKNRYICKQOL 178

RESULT 9
Q9NZS1
ID Q9NZS1 PRELIMINARY; PRT; 181 AA.
AC Q9NZS1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Lectin-like receptor FL, splice variant 1 KLRFI-sl.
GN KLRFI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KLRFI, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
DR EMBL; AF175207; AAF37805.1; -.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CAE1E551 CRC64;

Query Match 16.7%; Score 171.5; DB 4; Length 181;

```



```

Query Match      15.6%; Score 161; DB 6; Length 165;
Best Local Similarity 29.1%; Pred No. 8.1e-09;
Matches 48; Conservative 25; Mismatches 66; Indels 26; Gaps 7;

QY 40 MVALGLLVIL-----MSLLMYQRIICGSKDSTCSHCPS-----CPILWTRNGSHCY 87
Db 5 MIISGLIIVVLKIVGMTFFLLYFQIF--GS--SNVSPTPTESFGTVCTGWDHFHQGRCF 60

QY 88 YFSMEKKDWNSSLKFCADKGSLLTFFPDNQGVKLFGEYLQDPFYWIGLRNIDG---WEWE 144
Db 61 FLSTSENSWNNSMNFCKQKGSFLAIVNTPTEKLFQNTSGAEKYFIFGLLYQPAEKMMWEWI 120

QY 145 GGPALSLRILNLSLQRCGAHNRGL-----QASCEVALQWICKK 185
Db 121 NNSVFNGSVISHSHNFNCVTI--GLTKTFDAASCDVNYRSICEK 162

```

Search completed: August 10, 2004, 16:44:03
Job time : 33 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:35:35 ; Search time 47.5 Seconds
(without alignments)
1118.293 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSYSTLELPEAPQVD.....GLQASCEVALQWICKVLY 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1082526

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1029	100.0	188	4	AAE11760 Mouse mas
2	838	81.4	188	2	AAR77033 Mammalian
3	838	81.4	188	2	AAW88277 Rat mast
4	838	81.4	188	4	AAE11761
5	551	53.5	114	2	AAR77472 Partial s
6	222.5	21.6	99	2	AAW88267 Human MAF
7	178.5	17.3	179	2	AAW64791 Human Kp4
8	178.5	17.3	179	2	AAW40222 CD94. 7/1
9	178.5	17.3	179	8	ADP76965
10	167.5	16.3	142	4	AAW80296
11	167.5	16.3	142	6	ABG72616
12	167.5	16.3	160	4	AAW80302
13	160.5	15.6	181	2	AAW72288 Human G52
14	160.5	15.6	181	7	ADC38664 Human sec
15	156	15.2	182	4	AAU19660 Human nov
16	156	15.2	182	5	ABP47880 Human pol
17	156	15.2	182	7	ADC10842 Human ext
18	154	15.0	165	4	AAU00673 Human INT
19	154	15.0	165	6	ABO32541 Secreted
20	148.5	14.4	94	4	AAU19816 Human nov
21	148.5	14.4	94	5	ABP48036 Human pol
22	148.5	14.4	94	7	ADC10998 Human nov
23	148.5	14.4	140	4	AAU19836 Human nov
24	148.5	14.4	140	4	AAU19690 Human nov
25	148.5	14.4	140	4	ABBI5422 Human ner

ALIGNMENTS

RESULT 1

AAE11760
ID AAE11760 standard; protein; 188 AA.
XX AC AAE11760;
XX AC AAE11760;
DT 18-DEC-2001 (first entry)
XX XX
DE Mouse mast cell function associated antigen (MAFA) protein.
XX XX
KW Mouse; pharmaceutical composition; mast cell function associated antigen;
KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KW immunosuppressive; cytostatic.
XX OS Mus sp.
XX XX
XX XX
PH Key Location/Qualifiers
FT Domain 64..188
FT /note= "Extracellular domain"
XX XX
XX WO200170805-A2.
XX XX
XX XX
PD 27-SEP-2001.
XX XX
XX 16-MAR-2001; 2001WO-US008596.
XX XX
XX 17-MAR-2000; 2000US-0190716P.
XX XX
XX (GEMI-) GEMINI SCI INC.
XX Takahashi N, Mikayama T;
XX WFI; 2001-611482/70.
DR N-PSDB; AADI8735.
XX XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
XX XX
XX Example 1; Page 19; 49pp; English.
XX XX
XX The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical

26 148.5 14.4 140 4 ABB17909
27 148.5 14.4 140 5 ABP48056
28 148.5 14.4 140 5 ABP47910
29 148.5 14.4 140 7 ADC10872
30 148.5 14.4 140 7 ADC11018
31 148 14.4 149 2 AAW36957
32 147 14.3 35 4 AAM14192
33 147 14.3 35 4 ABB31139
34 147 14.3 35 4 AAM26602
35 147 14.3 35 4 ABB27967
36 147 14.3 35 4 ABB18604
37 147 14.3 35 4 AAM66323
38 147 14.3 35 4 AAM53935
39 147 14.3 35 4 ABG47989
40 147 14.3 35 4 AAM01928
41 147 14.3 35 5 ABG35971
42 145 14.1 145 6 AAU00675
43 145 14.1 145 6 ABO32547
44 145 14.1 146 4 AAM25760
45 144.5 14.0 146 4 AAM51544

Abb17909 Human ner
Abp48056 Human pol
Abp47910 Human pol
Adc10872 Human ext
Adc11018 Human pro
Aaw36957 Protein e
Aam14192 Peptide #
Abb31139 Peptide #
Aam26602 Peptide #
Abb27967 Human pep
Abb18604 Protein #
Aam66323 Human bon
Aam53935 Human bra
Abg47989 Human liv
Aam01928 Peptide #
Abg35971 Human pep
Aau00675 Human INT
Abo32547 Secreted
Aam25760 Human pro
Aam51544 Snake ven

CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is mouse MAFA protein
 XX
 SQ Sequence 188 AA;

Query Match 100.0%; Score 1029; DB 4; Length 188;
 Best Local Similarity 100.0%; Pred. No. 6.6e-103;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MADSSYSTLELPEAPOQVDSRWKLVKAVLHRPHLSRFAMVALGLTIVILMSLLMYQRIL 60
 Db 1 MADSSYSTLELPEAPOQVDSRWKLVKAVLHRPHLSRFAMVALGLTIVILMSLLMYQRIL 60
 Qy 61 CCGSKDSTCSHCPCPILWTRNGSHCYFVSMEKDWNSLKFCDKSGSHLLTFPDNGVK 120
 Db 61 CCGSKDSTCSHCPCPILWTRNGSHCYFVSMEKDWNSLKFCDKSGSHLLTFPDNGVK 120
 Qy 121 LFGEYLGQDFYWGIRNIDGWRWEGGPPALSRLITNSLIQRCGAHNRGLQASCEVALQ 180
 Db 121 LFGEYLGQDFYWGIRNIDGWRWEGGPPALSRLITNSLIQRCGAHNRGLQASCEVALQ 180
 Qy 181 WICKKVL 188
 Db 181 WICKKVL 188

RESULT 2

AAAR77033
 ID AAR77033 standard; protein; 188 AA.

AC AAR77033;
 XX

DT 01-FEB-1996 (first entry)

DE Mammalian mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA; soluble; ligand;
 KW identification; screening; inflammation; inflammatory; allergy; allergic;
 KW prevention.

XX Rattus rattus.
 OS

XX WO9527734-A1.
 PN

XX 19-OCT-1995.
 PD

XX 06-APR-1995; 95WO-US004258.
 PF

XX 08-APR-1994; 94IL-00109257.
 PR

XX (YEDA) YEDA RES & DEV CO LTD.
 PA

XX (RYCU/) RYCU A.
 PA

XX Pecht I, Guthmann MD, Tal M;
 PI

XX WPI; 1995-366356/47.
 DR

XX N-PSDB; AAT01471.
 DR

XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
 PT useful for screening for ligands of MAFA which are useful for prevention
 PT of inflammatory and allergic reactions.

XX Claim 12; Page 37; 54pp; English.
 PS

XX A soluble form of mast cell function-associated antigen (MAFA) can be
 CC produced by recombinant techniques for use in the ligand- screening
 CC assay. The ligands that are identified may be used alone or in

CC combination with the MAFA to prevent inflammatory and allergic reactions
 XX
 SQ Sequence 188 AA;

Query Match 81.4%; Score 838; DB 2; Length 188;
 Best Local Similarity 80.7%; Pred. No. 3.2e-82;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MADSSYSTLELPEAPOQVDSRWKLVKAVLHRPHLSRFAMVALGLTIVILMSLLMYQRIL 60
 Db 1 MADNSIYSTLELPEAPRVQDDSRWKVAVLHRPCVSYLVVVALGLTIVILMSLLYQRTL 60
 Qy 61 CCGSKDSTCSHCPCPILWTRNGSHCYFVSMEKDWNSLKFCDKSGSHLLTFPDNGVK 120
 Db 61 CCGSKGFMCSQCPCPNLWNRNGSHCYFVSMEKDWNSLKFCDKSGSHLLTFPDNGVN 120
 Qy 121 LFGEYLGQDFYWGIRNIDGWRWEGGPPALSRLITNSLIQRCGAHNRGLQASCEVALQ 180
 Db 121 LFQYVGEDFYWIGLRIDGWRWEDGPALSLILSNVYQCKGTHRCGLHASSCEVALQ 180
 Qy 181 WICKKVL 187
 Db 181 WICKKVL 187

RESULT 3

AAW88277
 ID AAW88277 standard; protein; 188 AA.

XX AC AAW88277;
 XX

XX 29-MAR-1999 (first entry)
 DT

XX Rat mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA; splice variant; rat;
 KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

XX Rattus sp.
 OS

XX Key Location/Qualifiers
 FH Modified-site 82.84

FT /note= "Asn is N-glycosylated"

FT Modified-site 97.99

FT /note= "Asn is N-glycosylated"

XX WO9854209-A2.
 PN

XX 03-DEC-1998.
 PD

XX 29-MAY-1998; 98WO-GB001572.
 PF

XX 31-MAY-1997; 97GB-00011148.
 PR

XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
 PA

XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
 PI

XX WPI; 1999-059806/05.
 DR

XX N-PSDB; AAV84222.
 DR

XX New polypeptide having a sequence corresponding to human mast cell
 PT function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.

XX Disclosure; Fig 4; 44pp; English.
 PS

XX This is the amino acid sequence of rat mast cell function-associated
 CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and
 CC basophils. The invention relates to cloning of the human MAFA molecule
 CC (see AAW88265) and to the discovery of splice variants (see AAW88266-67)
 CC of human MAFA that are not found in rat. Polypeptides and synthetic

CC peptides (see AAW88258-64) based on human MAFA and human truncated MAFA,
 CC and polynucleotides encoding them, can be used in methods for the
 CC treatment of inflammatory and allergic diseases (e.g. rheumatoid
 CC arthritis and asthma), and tumour growth
 XX
 SQ Sequence 188 AA;

Query Match 81.4%; Score 838; DB 2; Length 188;
 Best Local Similarity 80.7%; Pred. No. 3.2e-82;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
 QY 1 MADSSYSTLELPEAPOQVDESRLKAVLHRLPHLSRFAMVALGLLTVILMSLLMYOKIL 60
 Db 1 MADNSYSTLELPAAPRVQDSSRWKAVLHRLPCVSVLVVVALGLLTVILMSLLLYORTL 60
 QY 61 CCGSKDSTCHSCSPILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTTPDNGVK 120
 Db 61 CCGSKGPMCSQCRCFNLWRNGSHCYFFSMKKDWNSSLKFCADKGSLLTTPDNGVN 120
 QY 121 LFGELYGQDFYWGILRNIDGWRWEGGPAISLRLITNSLIQRCGAIHNGIQAASCEVALQ 180
 Db 121 LFGELYGQDFYWGILRNIDGWRWEGGPAISLRLITNSLIQRCGAIHNGIQAASCEVALQ 180
 QY 181 WICKKVL 187
 Db 181 WICKKVL 187

RESULT 4
 AAE11761
 ID AAE11761 standard; protein; 188 AA.
 AC AAE11761;
 DT 18-DEC-2001 (first entry)
 XX
 DE Rat mast cell function associated antigen (MAFA) protein.
 XX
 DE Rat; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 XX
 OS Rattus norvegicus.
 XX
 PN WC200170805-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 16-MAR-2001; 2001WO-US008596.
 XX
 PR 17-MAR-2000; 2000US-0190716P.
 XX
 PA (GEMI-) GEMINI SCI INC.
 XX
 PI Takahashi N, Mikayama T;
 XX
 DR WPI; 2001-611482/70.
 DR N-PSDB; AAD18736.
 XX
 PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX
 PS Example 1; Page 19; 49pp; English.

XX The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition

CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is rat MAFA protein
 XX
 SQ Sequence 188 AA;

Query Match 81.4%; Score 838; DB 4; Length 188;
 Best Local Similarity 80.7%; Pred. No. 3.2e-82;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
 QY 1 MADSSYSTLELPEAPOQVDESRLKAVLHRLPHLSRFAMVALGLLTVILMSLLMYOKIL 60
 Db 1 MADNSYSTLELPAAPRVQDSSRWKAVLHRLPCVSVLVVVALGLLTVILMSLLLYORTL 60
 QY 61 CCGSKDSTCHSCSPILWTRNGSHCYFFSMKKDWNSSLKFCADKGSLLTTPDNGVK 120
 Db 61 CCGSKGPMCSQCRCFNLWRNGSHCYFFSMKKDWNSSLKFCADKGSLLTTPDNGVN 120
 QY 121 LFGELYGQDFYWGILRNIDGWRWEGGPAISLRLITNSLIQRCGAIHNGIQAASCEVALQ 180
 Db 121 LFGELYGQDFYWGILRNIDGWRWEGGPAISLRLITNSLIQRCGAIHNGIQAASCEVALQ 180
 QY 181 WICKKVL 187
 Db 181 WICKKVL 187

RESULT 5
 AAR77472
 ID AAR77472 standard; protein; 114 AA.
 AC AAR77472;
 DT 01-FEB-1996 (first entry)
 XX
 DE Partial sequence of mast cell function-associated antigen (MAFA).
 XX
 KW Mast cell function-associated antigen; MAFA; soluble; ligand;
 KW identification; screening; inflammation; inflammatory; allergy; allergic;
 KW prevention.
 XX
 OS Rattus rattus.
 XX
 PN WC9527734-A1.
 XX
 PD 19-OCT-1995.
 XX
 PF 06-APR-1995; 95WO-US004258.
 XX
 PR 08-APR-1994; 94IL-00109257.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (RYCU/) RYCUS A.
 XX
 PI Pecht I, Guthmann MD, Tal M;
 XX
 DR WPI; 1995-366356/47.
 DR N-PSDB; AAT01471.

XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
 PT useful for screening for ligands of MAFA which are useful for prevention
 PT of inflammatory and allergic reactions.

XX Disclosure; Page 38; 54pp; English.

XX A soluble form of mast cell function-associated antigen (MAFA) can be
 CC produced by recombinant techniques for use in the ligand- screening
 CC assay. The ligands that are identified may be used alone or in
 CC combination with the MAFA to prevent inflammatory and allergic reactions

```

XX SQ Sequence 114 AA;
Query Match 53.5%; Score 551; DB 2; Length 114;
Best Local Similarity 84.1%; Pred. No. 1.9e-51;
Matches 95; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 75 CPILWTRNGSHCYFYSMEKDWNSLKFCADKSGHLLTFPDNQGVKLFGEYLGDFYWG 134
Db 1 CPNLWNRNGSHCYFYSMEKDWNSLKFCADKSGHLLTFPDNQGVNLFQEVGDFYWG 60

QY 135 LRNIDGWRWEGGPPALSRLITNSLIQRCGAHNRNGLOASSCEVALQWICKVL 187
Db 61 LRIDGWRWEDGPALSRLITNSLVVQKGTTHRCGLHASSCEVALQWICKVL 113

RESULT 6
AAW88267
ID AAW88267 standard; protein; 99 AA.
XX AC
XX AC AAW88267;
XX DT
XX DT 29-MAR-1999 (first entry)
XX DE
XX DE Human MAFa splice variant huMAFA(E3/4-).
XX KW Mast cell function-associated antigen; MAFa; huMAFA(E3/4-);
XX KW splice variant; human; inflammation; allergy; asthma;
XX KW rheumatoid arthritis; tumour; therapy.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO9854209-A2.
XX PD
XX PD 03-DEC-1998.
XX PF
XX PF 29-MAY-1998; 98WO-GB001572.
XX PR
XX PR 31-MAY-1997; 97GB-00011148.
XX PA
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI
XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX DR
XX DR WPI: 1999-059806/05.
XX DR N-PSDB; AAV84200.
XX PT
XX PT New polypeptide having a sequence corresponding to human mast cell
XX PT function-associated antigen - useful in forming and manufacturing
XX PT pharmaceutical compositions in the treatment of inflammatory and allergic
XX PT diseases, and tumour growth.
XX PS
XX PS Disclosure; Fig 3; 44pp; English.
XX CC
XX CC This is the amino acid sequence of human mast cell function- associated
XX CC antigen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-
XX CC like domain of human MAFa (see AAW88265) but retains the intracellular
XX CC and transmembrane domains as well as the extracellular C-terminal tail.
XX CC Truncated MAFa polypeptides including huMAFA(E3/4-), and polynucleotides
XX CC encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-
XX CC 72), can be used in compositions for the treatment of
XX CC inflammatory and allergic diseases (e.g. rheumatoid arthritis and
XX CC asthma), or tumour growth
XX SQ Sequence 99 AA;
Query Match 21.6%; Score 222.5; DB 2; Length 99;
Best Local Similarity 30.1%; Pred. No. 5.9e-16;
Matches 56; Conservative 13; Mismatches 28; Indels 89; Gaps 1;

QY 1 MADSSYSTLELPEAPQVQDESRLKAVLHRLPHSLRFAMVALGLTIVLMSLLMYQRL 60
Db 1 MTDVSYMSLELPTATQANDYGFQOKSSSRPSCSLVAIALGLTAVLLSYQLL 60

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QY 61 CCGSKDSTGCHPCPILWTRNGSHCYFYSMEKDWNSLKFCADKSGHLLTFPDNQGVK 120
Db 61 CCG----- 63
QY 121 LFGEYLGDFYWGILNRNIDGWRWEGGPPALSRLITNSLIQRCGAHNRNGLOASSCEVALQ 180
Db 64 -----ISSNSFVQTCGAIITKNGLOASSCEVPLH 91
QY 181 WICKKV 186
Db 92 WVCKKV 97

RESULT 7
AAW64791
ID AAW64791 standard; protein; 179 AA.
XX AC
XX AC AAW64791;
XX DT
XX DT 23-NOV-1998 (first entry)
XX DE
XX DE Human Kp43 protein.
XX KW Kp43; human; natural killer cell surface antigen; NK; T cell; inhibitor;
XX KW cell-mediated cytotoxicity; transplant rejection; autoimmune disease.
XX OS
XX OS Homo sapiens.
XX PN
XX PN US5811284-A.
XX PD
XX PD 22-SEP-1998.
XX PF
XX PF 20-MAY-1996; 96US-00650578.
XX PR
XX PR 29-DEC-1993; 93US-00175339.
XX PA
XX PA (SCHE ) SCHERING CORP.
XX PA (LOPEZ/) LOPEZ-BOTET M.
XX PA (BELT/) BELTRAN J A.
XX PI
XX PI Lanier LL, Chang C, Lopez-Botet M, Beltran JA, Phillips JH;
XX DR
XX DR WPI: 1998-530877/45.
XX DR N-PSDB; AAV46476.
XX PT
XX PT DNA encoding natural killer cell surface antigen Kp43 - and transformed
XX PT cells for producing recombinant Kp43.
XX PS
XX PS Claim 1; Col 31-32; 17pp; English.
XX CC
XX CC This sequence represents a novel human natural killer (NK) cell surface
XX CC antigen, Kp43. This sequence can be used in a method resulting in the
XX CC production of recombinant protein expressed by NK and T cells, which may
XX CC inhibit cell-mediated cytotoxicity, e.g. in transplant rejection or
XX CC autoimmune diseases, or may be used to produce antibodies for diagnostic
XX CC or therapeutic use
XX SQ Sequence 179 AA;
Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 7.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLTIVLMSLLMYQRLCCGS-----KDSTGCHPCPILWTRNGS 84
Db 14 GTLGIICLSMATLGLIKNSFTKLSIBPAFTPGNIELQKSDC--C-SCQEKWGYRC 70
QY 85 HCYFYSMEKDWNSLKFCADKSGHLLTFPDNQGVKLFGEYLGDFYWGILNRNID--GW 141
Db 71 NCYFISSEQKTWNESRHLCAQSKSLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGPPALSRLITN---SLIQRCGAHNRNG-LOASSCEVALQWICKKV 187

```

Db 129 LWNGSALSQYLFPSPFTNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 8

AAW40222
ID AAW40222 standard; peptide; 179 AA.

XX AC AAW40222;

DT 07-JUL-1998 (first entry)

XX CD94.

XX TMAH; apoptosis; osteoarthritis; diagnosis; treatment.

XX Homo sapiens.

XX WO9804585-A2.

XX 05-FEB-1998.

XX 22-JUL-1997; 97WO-US013077.

XX 31-JUL-1996; 96US-00690095.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Au-Young J, Goli SK;

XX WPI; 1998-130617/12.

XX Human macrophage antigen - used for decreasing apoptosis associated with
XX osteoarthritis.

XX Disclosure; Page 47; 58pp; English.

XX The type II integral membrane proteins (AAW40219-W40221) and CD94
XX antigen (TMAH) (AAW40215). The homology which TMAH shares with this group
XX includes a series of disulphide residues. The structural homology between
XX the peptides provides information on the structural and physical
XX properties of both the TMAH gene and protein. This is used in the
XX development of TMAH as a diagnostic tool and as a method of treating
XX diseases associated with expression of TMAH

XX Sequence 179 AA;

Query Match 17.3%; Score 178.5; DB 2; Length 179;

Best Local Similarity 31.8%; Pred. No. 7.5e-11;

Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLTIVILMSLLMQRIILCCGS-----KSTCSHCSPCPILWTRNGS 84

Db 14 GTLGIICLSLMATIGILLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SCQEKWVGRC 70

QY 85 HCYVFSMEKKDWNSSLKFCADKSGHLLTFPDNQGVKLFGEYLQDFWIGLRNID----GW 141

Db 71 NCYFISSEQKTNWESHRLCASQKSSLLQLQNTDLEDFMSS--SQQFYWIGLSYSEHTAW 128

QY 142 RWEGGPALSRLITN----SLIQRCGAHRNG-LQASSCEVALQWICKKVL 187

Db 129 LWNGSALSQYLFPSPFTNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 9

ADE76965
ID ADE76965 standard; protein; 179 AA.

XX AC ADE76965;

XX 29-JAN-2004 (first entry)

XX

Human protein expressed in a liver disorder #36.

human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
tumour; liver; inflammatory disorder; immune response disorder;
high-throughput screening; differential gene expression; gene therapy.

Homo sapiens.

US2003108871-A1.

12-JUN-2003.

30-JUL-2001; 2001US-00919039.

28-JUL-2000; 2000US-0222113P.

(KASE/) KASER M R.

Kaser MR;

WPI; 2004-031227/03.

N-PSDB; ADE76964.

Composition comprising several cDNAs that are differentially expressed in
treated human C3A liver cell cultures, useful for treating liver
disorders.

Claim 1; SEQ ID NO 130; 41pp; English.

The invention relates to a composition comprising several cDNAs that are
differentially expressed in a liver disorder. The composition is useful
for treating liver disorder such as hyperlipidaemia, hypertension, type
II diabetes, tumours of the liver and disorders of the inflammatory and
immune response. The composition is useful for a high-throughput method
of screening several molecules or compounds to identify a ligand which
specifically binds a cDNA. A protein encoded by the cDNA is useful for a
high-throughput method for using a protein to screen several molecules or
compounds to identify at least one ligand which specifically binds the
protein which involves combining the protein encoded by the cDNA with
several of molecules or compounds under conditions to allow specific
binding, and detecting specific binding between the protein and a
molecule or compound, therefore identifying a ligand which specifically
binds the protein. The composition is useful for detecting and
quantifying differential gene expression, can be used in gene therapy, to
formulate prognosis and to design a treatment regimen and to monitor the
efficacy of treatment. The present sequence represents the amino acid
sequence of a protein encoded by a cDNA differentially expressed in a
liver disorder.

Sequence 179 AA;

Query Match 17.3%; Score 178.5; DB 8; Length 179;

Best Local Similarity 31.8%; Pred. No. 7.5e-11;

Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLTIVILMSLLMQRIILCCGS-----KSTCSHCSPCPILWTRNGS 84

Db 14 GTLGIICLSLMATIGILLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SCQEKWVGRC 70

QY 85 HCYVFSMEKKDWNSSLKFCADKSGHLLTFPDNQGVKLFGEYLQDFWIGLRNID----GW 141

Db 71 NCYFISSEQKTNWESHRLCASQKSSLLQLQNTDLEDFMSS--SQQFYWIGLSYSEHTAW 128

QY 142 RWEGGPALSRLITN----SLIQRCGAHRNG-LQASSCEVALQWICKKVL 187

Db 129 LWNGSALSQYLFPSPFTNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 10

AAW80296

ID AAW80296 standard; protein; 142 AA.

XX AC AAW80296;

PS Claim 8; Page 59; 81pp; English.

XX This sequence represents a novel secreted protein, G52-24, isolated from

CC a clone, G52-24 (ATCC 98028), derived from a human PBMC cDNA library. The

CC nucleic acid and encoded G52-24 secreted protein can be used for research

CC purposes (as markers for tissues, molecular weight markers for gels,

CC primers, probes, etc.), for nutrition (as C, N or carbohydrate source),

CC as a cytokine for cell proliferation and differentiation activity, as

CC immune stimulants or suppressors e.g. for viral, bacterial or fungal

CC infections, for autoimmune diseases such as multiple sclerosis or

CC systemic lupus erythematosus, to regulate haematopoiesis, for tissue

CC growth, as an activin or inhibin, or having chemotactic, chemokinetic,

CC haemostatic and thrombolytic, receptor/ligand, anti-inflammatory or

CC tumour inhibitory activities

XX

SQ Sequence 181 AA;

Query Match 15.6%; Score 160.5; DB 2; Length 181;

Best Local Similarity 26.8%; Pred. No. 6.8e-09;

Matches 42; Conservative 19; Mismatches 67; Indels 29; Gaps 5;

QY 50 LMSLLMYQRIICCG-----SKDSTCSHCPs-----CPILWTRNGSHCYFSEMKKDW 97

Db 28 LFFLLMELTIIICGVMVAALSAIRANCHQEPSVCLQAACPESWIGFQKCFYFSDDTKNWT 87

QY 98 SSLKFCADKGSHELLTFPNQGVKLFGEYLQDFYWGILRNIDG--WRWEGG-----PA 148

Db 88 SSQRFCSDQADLAQVESFOELNFLRYKGPSDHWIGLSREGQGPWKWINGTEWTRQFPI 147

QY 149 LSLRLITNSLIQRCGAIHRNGIQASSCEVALQWICK 185

Db 148 LG-----AGECAYLNDKGASSARHYTERKWICK 176

RESULT 14

ID ADC38664

XX ADC38664 standard; protein; 181 AA.

AC ADC38664;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human secreted protein #11.

XX

KW immune disorder; severe combined immunodeficiency; SCID;

KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;

KW rheumatoid arthritis; allergic reaction; asthma; myeloid cell deficiency;

KW lymphoid cell deficiency; osteoporosis; osteoarthritis;

KW peripheral nervous system disease; peripheral neuropathy;

KW Alzheimer's disease; Parkinson's disease; coagulation disorder;

KW inflammatory disease; systemic inflammatory response syndrome; SIRS;

KW ischaemia-reperfusion injury; Crohn's disease; anaphylaxis; fertility;

KW hypersensitivity; regeneration; neural cell proliferation; tumour;

KW tumour; chemokine; human; secreted protein.

XX

OS Homo sapiens.

XX

PN US2002193567-A1.

XX

PD 19-DEC-2002.

XX

PF 02-APR-2002; 2002US-00114893.

XX

PR 11-AUG-1995; 95US-00514014.

PR 05-APR-1996; 96US-00628364.

PR 19-APR-1996; 96US-00635311.

PR 07-JUN-1996; 96US-00659224.

PR 17-JUN-1996; 96US-00664596.

PR 09-JUL-1996; 96US-00677231.

PR 26-JUL-1996; 96US-00686878.

PR 23-AUG-1996; 96US-00701819.

PR 27-SEP-1996; 96US-00721488.

PR 27-SEP-1996; 96US-00721798.

27-SEP-1996; 96US-00721923.

PR 27-SEP-1996; 96US-00721926.

PR 25-OCT-1996; 96US-00738367.

PR 30-OCT-1996; 96US-00739775.

PR 13-JAN-1997; 97US-00783395.

PR 10-APR-1997; 97US-00833823.

PR 02-JUN-1997; 97US-00867677.

PR 05-SEP-1997; 97US-00924838.

PR 06-OCT-1999; 99US-00413232.

XX (GEMY) GENETICS INST INC.

FA Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

XX Meiberg D, Treacy M, Bowman MR, Spaulding V, Carlin-Duckett M;

PI Kelleher K;

PI

XX WPI; 2003-657236/62.

DR N-PSDB; ADC38663.

XX

PT Proteins AZ3021 encoded by clone AZ3021 from human adult colon, and

PT BD12716 encoded by clone BD12716 from human fetal kidney cDNA library,

PT useful for treating e.g. multiple sclerosis and rheumatoid arthritis.

XX

PS Disclosure; SEQ ID NO 22; 412pp; English.

XX

CC The invention relates to a protein comprising fully defined AZ302 1

CC protein or BD127 1 6 protein. The polynucleotides are useful for

CC expressing recombinant proteins for analysis and are also useful as

CC chromosome markers or tags to identify chromosomes or to map related gene

CC positions. The proteins are useful as amino acid supplement, carbon

CC source, nitrogen source and carbohydrate source. The proteins are useful

CC for treating various immune deficiencies and disorders (e.g. severe

CC combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple

CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis), allergic

CC reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,

CC osteoporosis or osteoarthritis, peripheral nervous system diseases (e.g.

CC peripheral neuropathy, Alzheimer's disease, Parkinson's disease),

CC coagulation disorders, inflammatory diseases (e.g. systemic inflammatory

CC response syndrome (SIRS)), ischaemia-reperfusion injury, Crohn's disease),

CC anaphylaxis and hypersensitivity. Proteins are also useful for inducing

CC tumour immunity, for inducing bone, cartilage, tendon, ligament and/or

CC nerve growth or regeneration, for proliferating neural cells and for

CC regenerating nerve and brain tissue, for inducing fertility and for

CC inhibiting tumour growth. Proteins are also useful as chemokine for

CC mammalian cells (e.g., monocytes, fibroblasts, neutrophils), and also

CC useful as inhibitors of receptor/ligand interactions. The present

CC sequence represents the amino acid sequence of a human secreted protein.

XX

SQ Sequence 181 AA;

Query Match 15.6%; Score 160.5; DB 7; Length 181;

Best Local Similarity 26.8%; Pred. No. 6.8e-09;

Matches 42; Conservative 19; Mismatches 67; Indels 29; Gaps 5;

QY 50 LMSLLMYQRIICCG-----SKDSTCSHCPs-----CPILWTRNGSHCYFSEMKKDW 97

Db 28 LFFLLMELTIIICGVMVAALSAIRANCHQEPSVCLQAACPESWIGFQKCFYFSDDTKNWT 87

QY 98 SSLKFCADKGSHELLTFPNQGVKLFGEYLQDFYWGILRNIDG--WRWEGG-----PA 148

Db 88 SSQRFCSDQADLAQVESFOELNFLRYKGPSDHWIGLSREGQGPWKWINGTEWTRQFPI 147

QY 149 LSLRLITNSLIQRCGAIHRNGIQASSCEVALQWICK 185

Db 148 LG-----AGECAYLNDKGASSARHYTERKWICK 176

RESULT 15

AAU19660

ID AAU19660 standard; protein; 182 AA.

XX

AC AAU19660;

XX

DT 04-DEC-2001 (first entry)
XX Human novel extracellular matrix protein, Seq ID No 310.
DE
XX
XX Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV;
KW antianemic; antirheumatic; antisclerotic; cardiant; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;
KW antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
KW cancers; hyperproliferative disorder; breast neoplasm; melanoma;
KW Sezary syndrome; Gaucher's disease; neurological diseases;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW cardiac arrest; tachycardia; angina; infection; corneal infections;
XX wound healing; immunogen; gene therapy; anisense; food additive.
XX
OS Homo sapiens.
XX
XX WO200155368-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001348.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 01-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218230P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 18-AUG-2000; 2000US-0225759P.
PR 22-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 23-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
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PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
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PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
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PR 13-OCT-2000; 2000US-0239935P.
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PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
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PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246611P.
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PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
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PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
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PR 17-NOV-2000; 2000US-0249216P.
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PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
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PR 17-NOV-2000; 2000US-0249297P.
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PR 17-NOV-2000; 2000US-0249300P.

PR	01-DEC-2000;	2000US-0250150P.
PR	01-DEC-2000;	2000US-0250391P.
PR	05-DEC-2000;	2000US-0251030P.
PR	05-DEC-2000;	2000US-0251988P.
PR	05-DEC-2000;	2000US-0256719P.
PR	06-DEC-2000;	2000US-0251479P.
PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251989P.
PR	11-DEC-2000;	2000US-0251990P.
PR	11-DEC-2000;	2000US-0254097P.
PR	05-JAN-2001;	2001US-0259678P.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
DR		
XX	WPI; 2001-465572/50.	
DR	N-PSDB; AAS31231.	
XX		
PT	Nucleic acid molecules encoding human secreted extracellular matrix	
PT	proteins, used in preventing, treating or ameliorating a disorder, e.g.	
PT	Alzheimer's and Parkinson's diseases and cancers.	
XX		
XX	Claim 11; SEQ ID NO 310; 577pp; English.	
XX		
CC	The invention relates to isolated nucleic acid molecules encoding novel	
CC	human secreted extracellular matrix proteins (SPs). The polynucleotides	
CC	and proteins are used to prevent, treat a medical condition in e.g.	
CC	humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For	
CC	example, disorders associated with decreased expression of SPs. The SP	
CC	polynucleotide or a vector expressing them may be administered to treat	
CC	diseases by gene therapy. Antisense molecules may be administered to down	
CC	regulate expression of SPs by binding with the cells own genes and	
CC	preventing their expression. The polynucleotides may also be used as DNA	
CC	probes in diagnostic assays. The SPs may also be used as antigens to	
CC	produce antibodies and to identify modulators (agonists and antagonists)	
CC	of the SPs. The anti-(sp) antibodies and antagonists may also be used to	
CC	down regulate expression and activity of SP and as diagnostic agents for	
CC	detecting the presence of SPs in samples. The disorders include for	
CC	example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency	
CC	virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis),	
CC	cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of	
CC	the breast or liver, Sezary syndrome and Gaucher's disease), neurological	
CC	diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-	
CC	/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina),	
CC	infections caused by bacteria, viruses and fungi and ocular disorders	
CC	(e.g. corneal infections). Other uses include wound healing, maintenance	
CC	of organs before transplantation, support of cell culture of primary	
	Query Match	15.2%; Score 156; DB 4; Length 182;
	Best Local Similarity	29.2%; Pred. No. 2.le-08;
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Db	53 LCASRSADQTV-----LCQSEWLKYCKGYWFNSNMKWSDSYVYCERKSHLIIITDDLE 108	
	: : : :	
Qy	119 VKLFCEYLIGO-DFYWIGIRNID---GWWEQGPALSLRLI-----TNSLIQRCGATHR 167	
	: : : :	
Db	109 MAFTQKNJQLUNYVWIGNFTLSKMTWTVDGSPIDSFKFFTKGPAKENS-----CAAIKE 164	
	: : : :	
Qy	168 NGLQASSCEVALQWICK 184	
	: : : :	
Db	165 SKIFSETCSSVFVKIQ 181	
	: : : :	

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:44:06 ; Search time 39.5 Seconds
(without alignments)

1492.972 Million cell updates/sec

Title: US-09-811-367B-3

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Searched: 1291235 seqs, 313682936 residues

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Maximum Match 100%

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- 4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1029	100.0	188	9	US-09-811-367B-3
2	838	81.4	188	9	US-09-811-367B-5
3	178.5	17.3	179	10	US-09-919-039-130
4	178.5	17.3	179	15	US-10-335-009-10
5	160.5	15.6	181	13	US-10-114-893-22
6	156	15.2	182	9	US-09-764-870-310
7	156	15.2	182	14	US-10-125-540-310
8	154	15.0	165	10	US-09-759-130B-98
9	154	15.0	165	16	US-10-741-790-98
10	151	14.7	132	15	US-10-335-009-4
11	148.5	14.4	94	9	US-09-764-870-466
12	148.5	14.4	94	14	US-10-125-540-466
13	148.5	14.4	140	9	US-09-764-870-340
14	148.5	14.4	140	9	US-09-764-870-486
15	148.5	14.4	140	14	US-10-125-540-340

16	148.5	14.4	140	14	US-10-125-540-486	Sequence 486, App
17	147	14.3	35	9	US-09-864-761-33902	Sequence 33902, A
18	145	14.1	145	10	US-09-759-130B-108	Sequence 108, App
19	145	14.1	145	16	US-10-741-790-108	Sequence 108, App
20	145	14.1	146	12	US-10-296-115-1275	Sequence 1275, Ap
21	144	14.0	137	14	US-10-106-698-5855	Sequence 5855, Ap
22	144	14.0	149	10	US-09-284-320-11	Sequence 11, Appl
23	144	14.0	149	13	US-10-114-893-32	Sequence 32, Appl
24	144	14.0	149	14	US-10-088-859-2	Sequence 2, Appl
25	144	14.0	149	14	US-10-179-528-1	Sequence 1, Appl
26	143.5	13.9	188	10	US-09-759-130B-83	Sequence 83, Appl
27	143.5	13.9	188	16	US-10-741-790-83	Sequence 83, Appl
28	143	13.9	149	9	US-09-944-807-6	Sequence 6, Appl
29	142	13.8	161	10	US-09-766-511B-55	Sequence 55, Appl
30	142	13.8	162	14	US-10-270-470-2	Sequence 2, Appl
31	140	13.6	138	10	US-09-759-130B-100	Sequence 100, App
32	140	13.6	138	16	US-10-741-790-100	Sequence 100, App
33	140	13.6	162	10	US-09-759-130B-85	Sequence 85, Appl
34	140	13.6	162	16	US-10-741-790-85	Sequence 85, Appl
35	137	13.3	187	10	US-09-759-130B-86	Sequence 86, Appl
36	137	13.3	187	16	US-10-741-790-86	Sequence 86, Appl
37	137	13.3	187	16	US-10-775-640-12	Sequence 12, Appl
38	135	13.1	133	12	US-10-239-656-3	Sequence 3, Appl
39	135	13.1	143	12	US-10-239-656-2	Sequence 2, Appl
40	135	13.1	162	12	US-10-239-656-90	Sequence 90, Appl
41	129.5	12.6	124	12	US-09-964-956-67	Sequence 67, Appl
42	129.5	12.6	124	12	US-10-072-012-836	Sequence 836, App
43	129.5	12.6	158	9	US-09-929-230-11	Sequence 11, Appl
44	129.5	12.6	158	14	US-10-226-420-11	Sequence 11, Appl
45	129	12.5	149	15	US-10-335-009-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Makayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAIST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-811-367B-3

Query Match 100.0%; Score 1029; DB 9; Length 188;
Best Local Similarity 100.0%; Pred. No. 7.9e-101;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MADSSYSTLELPEAPQVQDES	SWKLVLRHPLSRFAMVGLLTIVILMSLIMQRIIL	60
Db	1	MADSSYSTLELPEAPQVQDES	SWKLVLRHPLSRFAMVGLLTIVILMSLIMQRIIL	60
QY	61	CCGSKDSTCHSCPCILWTRNGSHCYFYSMEKWNNSLKF	CADKSGSHLLTTPDNGVK	120
Db	61	CCGSKDSTCHSCPCILWTRNGSHCYFYSMEKWNNSLKF	CADKSGSHLLTTPDNGVK	120
QY	121	LFGEYLQGFYWTGLRNLGDRWEGGPAISLRILTNLSL	IQRCGAIHRNGIQASCEVALQ	180
Db	121	LFGEYLQGFYWTGLRNLGDRWEGGPAISLRILTNLSL	IQRCGAIHRNGIQASCEVALQ	180

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QY 181 WICKKVL 188
Db 181 WICKKVL 188

RESULT 2
US-09-811-367B-5
; Sequence 5, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5

Query Match 81.4%; Score 838; DB 9; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.4e-80;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADSIYSTLELPEAPQVQDSRWKLVKAVLHRRPHLSRFAMVALGLLTVILMSLLMYQRL 60
Db 1 MADSIYSTLELPEAPQVQDSRWKLVKAVLHRRPHLSRFAMVALGLLTVILMSLLMYQRL 60

QY 61 CGSGKSDTSCSHCPILWTRNGSHCYFMSMEKKNSSLKFCADKGSLLTFPDNGQVK 120
Db 61 CGSGKGFMCQSCPCNLWNRNGSHCYFMSMEKKNSSLKFCADKGSLLTFPDNGQVK 120

QY 121 LFEYLGDFYWIGLNRIDGWEGGPPALSLRLTNSLIQRCGAHRNGLOASSCEVALQ 180
Db 121 LFEYVGDFYWIGLNRIDGWEGGPPALSLRLTNSLIQRCGAHRNGLOASSCEVALQ 180

QY 181 WICKKVL 187
Db 181 WICKKVL 187

RESULT 3
US-09-919-039-130
; Sequence 130, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 130
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 5163000CD1
US-09-919-039-130

Query Match 17.3%; Score 178.5; DB 10; Length 179;
Best Local Similarity 31.8%; Pred. No. 1.3e-10;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLTIVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIIICLSMATLGIILKNSFTKLSIEPAFTPGFNIELQKSDC--C-SCQEKWVGVC 70

QY 85 HCYYFSEMEKKNSSLKFCADKGSLLTFPDNGQVKLFGEYLGDFYWIGLNRID---GW 141
Db 71 NCYFISSEQKTWNSRHLCAQSKSSLQQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128

QY 142 RWEGGPALSLRLTN---SLIQRCAIHRNG--LQASSCEVALQWICKKVL 187
Db 129 LWENGSAISQYLFPSPFETFNKCIAYNPNGNALDESCEDEKKNRYICKQQL 178

RESULT 4
US-10-335-009-10
; Sequence 10, Application US/10335009
; Publication No. US20040001804A1
; GENERAL INFORMATION:
; APPLICANT: Forunelloor, Mathew A.
; APPLICANT: Boles, Kent S.
; TITLE OF INVENTION: LIT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE: 11707.02/469687-7
; CURRENT APPLICATION NUMBER: US/10/335,009
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-009-10

Query Match 17.3%; Score 178.5; DB 15; Length 179;
Best Local Similarity 31.8%; Pred. No. 1.3e-10;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLTIVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIIICLSMATLGIILKNSFTKLSIEPAFTPGFNIELQKSDC--C-SCQEKWVGVC 70

QY 85 HCYYFSEMEKKNSSLKFCADKGSLLTFPDNGQVKLFGEYLGDFYWIGLNRID---GW 141
Db 71 NCYFISSEQKTWNSRHLCAQSKSSLQQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128

QY 142 RWEGGPALSLRLTN---SLIQRCAIHRNG--LQASSCEVALQWICKKVL 187
Db 129 LWENGSAISQYLFPSPFETFNKCIAYNPNGNALDESCEDEKKNRYICKQQL 178

RESULT 5
US-10-114-893-22
; Sequence 22, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
```

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; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-22

Query Match      15.6%; Score 160.5; DB 13; Length 181;
Best Local Similarity 26.8%; Pred. No. 3.le-08;
Matches 42; Conservative 19; Mismatches 67; Indels 29; Gaps 5;

QY 50 LMSLLMYQRI LCCG-----SKDSTCSHCPS-----CPILWTRNGSHCYFYSMEKKDWN 97
Db 28 LFLIMFLTIIVCGMVAALSAIRANCHQEPSCVCLQAACPESWIGFQKCFYFSDDTKNWT 87
QY 98 SSLKFCADKSHLLTFPDNQGVKLFGYLGQDFWIGLRNIDG--WRWEGG-----PA 148
Db 88 SSORFCDSDADLAQVESFOELFLLRYKGPDSHWIGLSEEQGPQWIKNGTEWTRQFPI 147
QY 149 LSLRLITNSLIQRCGAIRHNGLOASSCEVALOWICK 185
Db 148 LG-----AGECAYLNDKGASSARHYTERKWICK 176

RESULT 6
US-09-764-870-310
; Sequence 310, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 310
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-310

Query Match      15.2%; Score 156; DB 9; Length 182;
Best Local Similarity 29.2%; Pred. No. 3.le-08;
Matches 40; Conservative 18; Mismatches 59; Indels 20; Gaps 6;

QY 60 LCCG-SKDSCTSCSPILWTRNGSHCYFYSMEKKDWNSSLKFCADKSGHLLTFPDNQ 118
Db 53 LCASRSADQTV-----LCQSEWLKYQKCYFWSNEMKSWSDSYVYCLERKSHLLIHDQLE 108
QY 119 VKLFGYLGQ-DFYWIGLRNID---GWRWEGGPALSRLIL-----TNSLIQRCGAHR 167
Db 109 MAFIQNLRQLNLYVWIGLNFSLKMTWTWVDGSPIDSKIFFIKGPAKENS-----CAAIKE 164
QY 168 NGLOASSCEVALOWICK 184
Db 165 SKIFSETCSSVFRWICQ 181

RESULT 7
US-10-125-540-310
; Sequence 310, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
US-10-125-540-310

Query Match      15.2%; Score 156; DB 14; Length 182;
Best Local Similarity 29.2%; Pred. No. 3.le-08;
Matches 40; Conservative 18; Mismatches 59; Indels 20; Gaps 6;

QY 60 LCCG-SKDSCTSCSPILWTRNGSHCYFYSMEKKDWNSSLKFCADKSGHLLTFPDNQ 118
Db 53 LCASRSADQTV-----LCQSEWLKYQKCYFWSNEMKSWSDSYVYCLERKSHLLIHDQLE 108
QY 119 VKLFGYLGQ-DFYWIGLRNID---GWRWEGGPALSRLIL-----TNSLIQRCGAHR 167
Db 109 MAFIQNLRQLNLYVWIGLNFSLKMTWTWVDGSPIDSKIFFIKGPAKENS-----CAAIKE 164
QY 168 NGLOASSCEVALOWICK 184
Db 165 SKIFSETCSSVFRWICQ 181

RESULT 8
US-09-759-130B-98
; Sequence 98, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: KIRST, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
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; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 340
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-340

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Query Match	14.4%;	Score 148.5;	DB 9;	Length 140;
Best Local Similarity	26.2%;	Pred. No. 1.4e-07;		
Matches	32;	Conservative 23;	Mismatches 64;	Indels 3; Gaps 3;

QY	69	CSHCPS-QPILITRNGSHCYFYSMEWKDNSSLKFCADKGSLLITFPDQGVKLFGEYL	127
Db	19	CIKCEAPCEDNLLYGRKCYFFSEEPDRDNTGRQYCHTHEAVLIATVOSKELEFMFKFTR	78
QY	128	QDFYWTIGLRNI-DGMEWEGGPALSLRILNSLTQRCGAIHRNGLOASSCEVALQWICKV	186
Db	79	RE-PWIGLRVGEFHVNGDPDPDTFTFIAGPGECVFVEPTRLVSTECMLTRPWCCKM	137
QY	187	LY 188	
Db	138	AY 139	

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RESULT 14
US-09-764-870-486
; Sequence 486, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-03-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 486
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-486

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Query Match	14.4%;	Score 148.5;	DB 9;	Length 140;
Best Local Similarity	26.2%;	Fred. No. 1.4e-07;		
Matches	32;	Conservative 23;	Mismatches 64;	Indels 3; Gaps 3;

QY	69	CSHCP	S-CFLLWTRNGSHCHYFESMEKKDWNSSLKFCADKGS	SHLLTFDPNQGVKLRCYIG	127
DB	19	CKCEAP	CPEDWLLYGRKCYFSEEPDPWNTGRQYCHTAEAVL	VIQSQLELFMKETR	78
QY	128	QDFYWIGLRNI	-DGRWEGGPALSRLITNSLIQRCGA	IHRNGLQASCEVALQWICKV	186
DB	79	RE-PWIGLR	RVCDPETHWNGDPDPDFTIAGPGECVF	ETRIWSTECMLTRPWC	137
QY	187	LY	188		
DB	138	AY	139		

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RESULT 15
US-10-125-540-340
; Sequence 340, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm

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; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 340
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-540-340

Query Match      14.4%; Score 148.5; DB 14; Length 140;
Best Local Similarity 26.2%; Pred. No. 1.4e-07;
Matches 32; Conservative 23; Mismatches 64; Indels 3; Gaps 3;

Qy 69 CSHCPSS-CPILWTRNGSHCYFESMEKKDWNSSLKFCADKGSLLLTFFPDNQGVLFGYLG 127
Db 19 CIKCEAPCPEDWLLYGRKCYFFSEPRDWTGROYCHTHEAVLAVIQSQKELEFEMFKETR 78

Qy 128 QDFYWIIGLRNI-DGWRWEGGPALSLRLITNSLIQRCGAHENGLOASCEVALQWICKKV 186
Db 79 RE-FWIGLRRYGDSEHFWNGDPFDDTFTIAGPGCEVFVEPTRLVSTECLEMTREPWCCKM 137

Qy 187 LY 188
Db 138 AY 139
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Search completed: August 10, 2004, 16:53:37
Job time : 41.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:40:40 ; Search time 14.5 Seconds
(without alignments)
669.357 Million cell updates/sec

Title: US-09-811-367B-3
Perfect score: 1029
Sequence: 1 MADSSIVTLELPAPQVQD.....GLQASSCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 303002

Minimum DB seq length: 0
Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB Length	ID	Description
1	838	81.4	188	3	US-08-722-126A-5	Sequence 5, Appli
2	838	81.4	188	5	PCT-US95-04258-5	Sequence 5, Appli
3	551	53.5	114	3	US-08-722-126A-6	Sequence 6, Appli
4	551	53.5	114	5	PCT-US95-04258-6	Sequence 6, Appli
5	267	25.9	76	4	US-09-531-056A-23	Sequence 23, Appli
6	178.5	17.3	179	1	US-08-690-095-9	Sequence 9, Appli
7	178.5	17.3	179	2	US-08-650-578-2	Sequence 2, Appli
8	178.5	17.3	179	2	US-08-688-342-3	Sequence 3, Appli
9	178.5	17.3	179	2	US-09-113-788-3	Sequence 3, Appli
10	178.5	17.3	179	3	US-09-113-789-9	Sequence 9, Appli
11	152	14.8	122	3	US-08-722-126A-9	Sequence 9, Appli
12	152	14.8	122	5	PCT-US95-04258-9	Sequence 9, Appli
13	150.5	14.6	115	3	US-08-722-126A-8	Sequence 8, Appli
14	150.5	14.6	115	5	PCT-US95-04258-8	Sequence 8, Appli
15	146	14.2	135	3	US-08-543-246B-19	Sequence 19, Appli
16	145	14.1	173	4	US-09-531-056A-4	Sequence 4, Appli
17	139.5	13.6	176	3	US-08-772-440-8	Sequence 8, Appli
18	139.5	13.6	180	3	US-08-772-440-31	Sequence 31, Appli
19	137	13.3	187	4	US-09-127-946-12	Sequence 12, Appli
20	136.5	13.3	129	3	US-08-722-126A-10	Sequence 10, Appli
21	136.5	13.3	129	5	PCT-US95-04258-10	Sequence 10, Appli
22	135	13.1	134	3	US-08-543-246B-20	Sequence 20, Appli
23	134.5	13.1	126	3	US-08-772-440-10	Sequence 10, Appli
24	134	13.0	120	3	US-08-543-246B-18	Sequence 18, Appli
25	134	13.0	135	3	US-08-543-246B-17	Sequence 17, Appli
26	133.5	13.0	77	4	US-09-531-056A-22	Sequence 22, Appli
27	132.5	12.9	79	4	US-09-531-056A-19	Sequence 19, Appli

28 127 12.3 77 4 US-09-531-056A-21 Sequence 21, Appli
29 127 12.3 78 4 US-09-531-056A-15 Sequence 15, Appli
30 127 12.3 78 4 US-09-531-056A-16 Sequence 16, Appli
31 125 12.1 78 4 US-09-531-056A-18 Sequence 18, Appli
32 124.5 12.1 117 1 US-07-614-443A-2 Sequence 2, Appli
33 124.5 12.1 117 1 US-08-294-859-2 Sequence 2, Appli
34 124.5 12.1 117 1 US-08-481-876-2 Sequence 2, Appli
35 124.5 12.1 123 5 PCT-US92-1034A-4 Sequence 4, Appli
36 124.5 12.1 123 5 PCT-US92-1034A-4 Sequence 4, Appli
37 120 11.7 149 4 US-09-489-847-167 Sequence 167, App
38 119 11.6 87 4 US-09-489-847-326 Sequence 326, App
39 119 11.6 107 1 US-07-893-929A-6 Sequence 6, Appli
40 119 11.6 107 5 PCT-US92-1034A-4 Sequence 6, Appli
41 117.5 11.4 168 3 US-08-772-440-17 Sequence 17, Appli
42 116 11.3 115 6 5514582-18 Patent No. 5514582
43 115 11.2 175 3 US-08-772-440-15 Sequence 15, Appli
44 114.5 11.1 125 1 US-07-893-929A-3 Sequence 3, Appli
45 114.5 11.1 125 5 PCT-US92-1034A-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-5

Query Match 81.4%; Score 838; DB 3; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.8e-86;

	Matches	151;	Conservative	15;	Mismatches	21;	Indels	0;	Gaps	0;
Qy	1	MADSSYSTLELPEAPQVDSRWKLVXALHRRPHLSRFAMVALGELLTVILMSLLMYQRIL	60							
Dd	1	MADNSIYSTLELPAAPRVDSDSRWKVKVLHRPCVSYLVMVALGLTIVILMSLLLYQRTL	60							
Qy	61	CCGSKDSTCHSPSCPTILTWRNGSHCYFFSMKKDWNSSLKFCADKGSHLLTFPDNQGKV	120							
Dd	61	CCGSKGPMCSQCSCPMLWNRNGSHCYFFSMEKEFDWNSSLKFCAKDGSHLLTFPDNQVN	120							
Qy	121	LFBEYLGODFWIGLRINDGWREGGPALSRLITNLRIORCGAIHRNGLOASSCEVALQ	180							
Dd	121	LFQEYGVEDFYWGIRDIIDGRWEDGGPALSISLINSNVQCKGTIHRCGLHASACEVALQ	180							
Qy	181	WICKKVL	187							
Dd	181	WICEKVL	187							

RESULT 2
 PCT-US95-04258-5
 ; Sequence 5, Application PC/TUS9504258
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
 ; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/04258
 ; FILING DATE: 06-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: IL 109257
 ; FILING DATE: 08-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: PECTHT=1 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 188 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-04258-5

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Qy 121 LFEYLGQDQYWTGLRNLIDGWRWEGGALSRLITNSLIQRCGAHHRNGLQASSCEVALQ 181
Db 121 LFOEYVGEDFYWTGLRDLIDGWRWEDGPALSILNSVYVQKCTIHRCGLHASSCEVALQ 180
Qy 181 WICKKVL 187
Db 181 WICKKVL 187

RESULT 3
US-08-722-126A-6
; Sequence 6, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/722,126A
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-6

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RESULT 4
PCT-US95-04258-6


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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,788
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/688,342
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
; US-09-113-788-3

Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYORILCCGS-----KDTCSHCPCPILWTRNGS 84
Db 14 GTLGIIICLSMATLGIILKNSFTKLSIEPAFTPGFNIELQKSDC--C-SQCKWVGRC 70

QY 85 HCYYFSMEKKDWNSSLKFCADKGSLLTFFPDNQVKLFGEVLGDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNEHRLCASQKSSLLQLONTDELFMSS--SQOFYWGILSYSEHTAW 128

QY 142 RWEGGPALSRLITN---SLIQRGAIHRNG-LQASCEVALOWICKKVL 187
Db 129 LWENGSSALSYLFPSEFTNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 10
US-09-113-789-9
; Sequence 9, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,789
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095
;

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,788
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/688,342
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
; US-09-113-788-3

Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYORILCCGS-----KDTCSHCPCPILWTRNGS 84
Db 14 GTLGIIICLSMATLGIILKNSFTKLSIEPAFTPGFNIELQKSDC--C-SQCKWVGRC 70

QY 85 HCYYFSMEKKDWNSSLKFCADKGSLLTFFPDNQVKLFGEVLGDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNEHRLCASQKSSLLQLONTDELFMSS--SQOFYWGILSYSEHTAW 128

QY 142 RWEGGPALSRLITN---SLIQRGAIHRNG-LQASCEVALOWICKKVL 187
Db 129 LWENGSSALSYLFPSEFTNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 10
US-09-113-789-9
; Sequence 9, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,789
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095
;

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
; US-09-113-789-9

Query Match 17.3%; Score 178.5; DB 3; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYORILCCGS-----KDTCSHCPCPILWTRNGS 84
Db 14 GTLGIIICLSMATLGIILKNSFTKLSIEPAFTPGFNIELQKSDC--C-SQCKWVGRC 70

QY 85 HCYYFSMEKKDWNSSLKFCADKGSLLTFFPDNQVKLFGEVLGDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNEHRLCASQKSSLLQLONTDELFMSS--SQOFYWGILSYSEHTAW 128

QY 142 RWEGGPALSRLITN---SLIQRGAIHRNG-LQASCEVALOWICKKVL 187
Db 129 LWENGSSALSYLFPSEFTNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 11
US-08-722-126A-9
; Sequence 9, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAPA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
;

```

REFERENCE/DOCKET NUMBER: PECHT-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-722-126A-9

Query Match 14.8%; Score 152; DB 3; Length 122;
Best Local Similarity 27.9%; Pred. No. 2e-09; Indels 8; Gaps 3;
Matches 34; Conservative 22; Mismatches 58; Indels 8; Gaps 3;
QY 75 CPILWTRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTFFPDNQGKLFGEYLGQDF--YW 132
Db 1 CPQDWLSHRDKCFHVSQVSNWTWEEGLVDCDCKGATMLIQOEELRFLDSIKKYNFSW 60
QY 133 IGLRNI---DQWRWEGGPALS---LRILTNSLIQRCGAHNRGLQASCEVALQWICKV 186
Db 61 IGLRYTLPDMNWKWINGSTLNSDLKGTDTENDSCAAISGDKVTFESCNSDNRWICQKE 120
QY 187 LY 188
Db 121 LY 122

RESULT 12
PCT-US95-04258-9
Sequence 9, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04258-9

Query Match 14.8%; Score 152; DB 5; Length 122;
Best Local Similarity 27.9%; Pred. No. 2e-09; Indels 8; Gaps 3;
Matches 34; Conservative 22; Mismatches 58; Indels 8; Gaps 3;
QY 75 CPILWTRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTFFPDNQGKLFGEYLGQDF--YW 132
Db 1 CPQDWLSHRDKCFHVSQVSNWTWEEGLVDCDCKGATMLIQOEELRFLDSIKKYNFSW 60
QY 133 IGLRNI---DQWRWEGGPALS---LRILTNSLIQRCGAHNRGLQASCEVALQWICKV 186
Db 61 IGLRYTLPDMNWKWINGSTLNSDLKGTDTENDSCAAISGDKVTFESCNSDNRWICQKE 120
QY 187 LY 188
Db 121 LY 122

RESULT 13
US-08-722-126A-8
Sequence 8, Application US/08722126A
Patent No. 6034227
GENERAL INFORMATION:
APPLICANT: PECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: UNITED STATES OF AMERICA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-722-126A-8

Query Match 14.6%; Score 150.5; DB 3; Length 115;
Best Local Similarity 26.3%; Pred. No. 2.8e-09; Indels 5; Gaps 3;
Matches 30; Conservative 20; Mismatches 59; Indels 5; Gaps 3;
QY 75 CPILWTRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTFFPDNQGKLFGEYLGQDFYWG 134
Db 1 CSEDWVGQYKCYFISTVTKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHWVG 60

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:39:40 ; Search time 13.5 Seconds
(without alignments)
1339.556 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSTLELPAPRVQD.....GLHASSCEVALQWICEKVLP 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 95185

Minimum DB seq length: 0
Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2 I59421	mast cell function
2	162.5	15.7	170	2 T28140	natural killer cell
3	158	15.3	156	2 T28141	C type lectin, B 1
4	146	14.1	146	2 JC7135	agkisactucin beta
5	137	13.2	167	1 WMVZF2	hepatic lectin hom
6	134.5	13.0	144	2 PC7027	aggreitin alpha cha
7	127.5	12.3	146	2 JC4691	coagulation factor
8	126	12.2	133	2 A47267	botroctetin alpha c
9	123.5	11.9	125	2 B47267	botroctetin beta ch
10	121.5	11.7	146	2 JC7105	aggreitin beta chai
11	115	11.1	123	2 B42972	coagulation factor
12	114.5	11.1	152	2 JC7134	agkisactucin alph
13	113	10.9	116	1 WMVZF8	hepatic lectin hom
14	112.5	10.9	162	1 LNRC3	lectin BRA3-2 prec
15	112	10.8	162	1 LNRC1	perlucin - Halioti
16	108.5	10.5	155	2 S78774	pancreatitits-assoc
17	103.5	10.0	175	2 A49616	coagulation factor
18	102.5	9.9	129	2 JC4329	regenerating islet
19	102	9.8	166	1 RGHU1A	pancreatic stone p
20	102	9.8	166	2 A45751	bitiscetin beta ch
21	100.5	9.7	125	2 JC5059	lectin, galactose-
22	100	9.7	135	2 A38609	pancreatic stone p
23	98	9.5	165	2 A28351	echicoidin - sea u
24	96.5	9.3	123	2 JC2415	coagulation beta cha
25	96.5	9.3	122	2 JC4690	regenerating islet
26	95	9.2	166	1 RGHU1B	pancreatitits-assoc
27	94.5	9.1	175	2 S29822	reg II, regenerati
28	94	9.1	173	2 B47148	pancreatitits-assoc
29	92.5	8.9	174	2 S54979	

30 92 8.9 175 2 A41719 pancreatic stone p
31 91 8.8 163 1 A34313 antifreeze protein
32 89.5 8.6 131 2 JC5058 bitiscetin alpha c
33 88 8.5 175 2 A37194 pancreatic thread
34 87 8.4 147 2 JC7938 type II antifreeze
35 87 8.4 153 2 T21396 hypothetical prote
36 87 8.4 173 2 S10548 lectin - barnacle
37 86 8.3 40 2 S56007 echinoidin - sea u
38 85 8.2 147 2 A26697 reg I, regeneratin
39 82 7.9 165 2 A47148 antifreeze protein
40 82 7.9 175 1 JH0626 ovocleidin - chick
41 81.5 7.9 142 2 S78596 hepatic lectin hom
42 81.5 7.9 143 1 WMVZEL regenerating prote
43 79 7.6 174 2 I83377 hypothetical prote
44 78.5 7.6 166 2 T28809 alboaaggregin-B alp
45 77 7.4 40 2 B56829

ALIGNMENTS

RESULT 1
I59421
mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I59421
R:Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A:Title: A secretion inhibitory signal transduction molecule on mast cells is another
A:Reference number: I59421; MUID:96016176; PMID:7568140
A:Accession: I59421
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-188 <RES>
A:Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C:Genetics:
A:Gene: mafa

Query Match 100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.2e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADNSIYSTLELPAPRVQDSDRWKVKAVLHRPCVSYLVNVALGLLTIVILMSLLLYQRTL 60
Db 1 MADNSIYSTLELPAPRVQDSDRWKVKAVLHRPCVSYLVNVALGLLTIVILMSLLLYQRTL 60
QY 61 CCGSKGFMCSQCRCPCNLWMRNGSHCYFYSMEKEDWNSSLKFCADKSGHLLTFPDQGVN 120
Db 61 CCGSKGFMCSQCRCPCNLWMRNGSHCYFYSMEKEDWNSSLKFCADKSGHLLTFPDQGVN 120
QY 121 LFOEYVGEDFYWTIGLRDIDGWRWEDGPALSLTSLNSVQKCGTIHRCGLHASSCEVALQ 180
Db 121 LFOEYVGEDFYWTIGLRDIDGWRWEDGPALSLTSLNSVQKCGTIHRCGLHASSCEVALQ 180
QY 181 WICEKVLP 188
Db 181 WICEKVLP 188

RESULT 2
T28140
natural killer cell receptor homolog - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T28140
R:Milne, S.; Kaufman, J.; Beck, S.
Submitted to the EMBL Data Library, May 1998
A:Description: DNA sequencing and analysis of the chicken major histocompatibility comp
A:Reference number: Z20475
A:Accession: T28140
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA

A;Residues: 1-170 <ML>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAA18960.1
A;Experimental source: clone cB12
C;Genetics:
A;Gene: B-NK
A;Map position: 16
A;Note: Intron positions not resolved (incomplete sequence)

Query Match 15.7%; Score 162.5; DB 2; Length 170;
Best Local Similarity 28.1%; Pred. No. 4.8e-08;
Matches 34; Conservative 16; Mismatches 60; Indels 11; Gaps 3;

QY 72 CSRCPNLMWRNGSHCYFSEMEKRDWNSLKFCAKDGSHLLTFPDNQGNLFOEYVGEDFY 131
Db 47 CLLCPQFWLLGDRCYELSTKGNWTQAKKCNLQSLAVLRKKAEDHLQWAGAEVP 106

QY 132 WIGLR-DIDGMRWEDGPAL-----LSILSNSVVKQGTTHRCGLHASSCEVALQWICEK 184
Db 107 WIGLEVSTNQKWDNSYNSSTEDNLVSMEN---RCGTFKTKVEGDVCSGEHQWVCQ 162

QY 185 K 185
Db 163 K 163

RESULT 3
T28141
C type lectin, B locus - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28141
R;Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex
A;Reference number: Z20475
A;Accession: T28141
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-156 <ML>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1
A;Experimental source: clone cB12
C;Genetics:
A;Gene: BLEC
A;Map position: 16
A;Introns: 17/1; 74/3; 110/2

Query Match 15.3%; Score 158; DB 2; Length 156;
Best Local Similarity 27.5%; Pred. No. 1.2e-07;
Matches 33; Conservative 22; Mismatches 55; Indels 10; Gaps 4;

QY 72 CSRCPNLMWRNGSHCYFSEMEKRDWNSLKFCAKDGSHLLTFPDNQGNLFOEYVGEDFY 131
Db 27 CAQCQFDWIGFKGKCYFSEDSNWTSSQNNCSALGASLAVFDSAEIDLSTWRHKGSSPH 86

QY 132 WIGLRDIDG---WRWEDGPALS--LSILSNSVVKQGTTHRCGLHASSCEVALQWICEK 185
Db 87 WVGL-SREGKEHPMEWNRSPSLHFLVQGDGL---CAYLGDAGLSSSHCSSTRNWNVCTK 142

RESULT 4
JC7135
agkiscutacin beta chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenolytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7135; PC7038
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7135
A;Molecule type: mRNA
A;Residues: 1-146 <CHE>

A;Cross-references: GB:AF176421
A;Experimental source: venom gland
A;Accession: PC7038
A;Molecule type: protein
C;Residues: 24-50;59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: agkiscutacin beta chain #status experimental <MAT>

Query Match 14.1%; Score 146; DB 2; Length 146;
Best Local Similarity 27.7%; Pred. No. 1.5e-06;
Matches 41; Conservative 19; Mismatches 50; Indels 38; Gaps 6;

QY 39 VMVALGELLTVILMSLLYQRTLCCSGKGFMCSCQSRCPNLMWRNGSHCYFSEMEKRDWNS 98
Db 5 IFVSFGLLVFLS-----LSGTAAADCPSEWSSVEGHCYKPFDFEPTWAD 48

QY 99 SLKFCAD--KGSHLLTFPDNQ-----VNLFOEYVGEDFYWIGLRDI-DG--WRWEDGPAL 149
Db 49 AEKFTQKHGKSHLASFHSSSEADFVVTLTTPSLKTLDLVWIGLKNWNGCYVKKWSGDTKL 108

QY 150 -----SLSILSNSVVKQCGT 164
Db 109 DYKDWREQFECLVSRVTNNWNLMSMDCGT 136

RESULT 5
WMVZF2
hepatic lectin homolog (BamHI-ORF2) - fowlpox virus (isolate HP-438 [Munich])
C;Species: fowlpox virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Accession: B29963
R;Tomley, F.; Binns, M.; Campbell, J.; Boursnell, M.
J. Gen. Virol. 69, 1025-1040, 1988
A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox virus
A;Reference number: JT0442; MUID:88229622; PMID:2836548
A;Accession: B29963
A;Molecule type: DNA
A;Residues: 1-167 <TOM>
A;Cross-references: GB:D00295; NID:g221380; PIDN:BAA00192.1; PID:g221383
C;Superfamily: fowlpox virus hepatic lectin homolog; C-type lectin homology
C;Keywords: early protein
F;49-152/Domain: C-type lectin homology <LCH>

Query Match 13.2%; Score 137; DB 1; Length 167;
Best Local Similarity 29.1%; Pred. No. 1.2e-05;
Matches 44; Conservative 21; Mismatches 78; Indels 8; Gaps 4;

QY 35 VSYLVVMVALGLTLVILMSLLYQRTLCCSGKGFMCSCQSRCPNLMWRNGSHCYFSEMEKR 94
Db 12 VSCYAITVLGILCLILFTILV---VVTCKVYVAFYFYSKVCPEDEWIGYNSKCYFTINET 68

QY 95 DWSLSLKFCADKGSHELLTFPDNQGNLFOEYVGEDFYWIGLRDIDGWEDGPALSIL 154
Db 69 NWNDSKGLCDVWDSLSLIRFDNIETLNFVSRV-GKGSYWI---DINQNRKIPGINFSL-YY 123

QY 155 SNSVVKQCGTTHRCGLHASSCEVALQWICEK 185
Db 124 EQVNDICLLPDTSNIEWSCIFHERTICVK 154

RESULT 6
PC7027
aggrelin alpha chain - Malayan pit viper (fragment)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C;Accession: PC7027
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggrelin, a collagen-like platelet
A;Reference number: PC7027; MUID:99443731; PMID:10512747
A;Accession: PC7027

C;Keywords: hemagglutinin; heterodimer; venom

F;2-121/Domain: C-type lectin homology <LCH>
F;2-13,30-121,98-113/Disulfide bonds: #status experimental
F;75/Disulfide bonds: interchain (to alpha-80) #status experimental

Query Match 11.9%; Score 123.5; DB 2; Length 125;
Best Local Similarity 31.3%; Pred. No. 0.00016;
Matches 26; Conservative 12; Mismatches 32; Indels 13; Gaps 4;

Qy 75 CPNLMWRNGSHCYFYSMEKRDWNSLKFCADK--GSHLLTFPDNQGNLFOEYVGE----- 128
Db 2 CPDPSSVEGHCYFFKFEWHEWDDAEFECTEQQTGAHLVSFQSKKEADFVRSLSLTSEMLKG 61

Qy 129 DFYWGILRDIDGM-----RWEDG 146

Db 62 DVVWIGLSDV--WNKCRFEWTDG 82

RESULT 10

JC7105

aggreitin beta chain - Malayan pit viper

C;Species: Calloselasma rhodostoma (Malayan pit viper)

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000

C;Accession: JC7105

R;Chung, C.H.; Au, L.C.; Huang, T.F.

Biochem. Biophys. Res. Commun. 263, 723-727, 1999

A;Title: Molecular cloning and sequence analysis of aggreitin, a collagen-like platelet a

A;Reference number: JC7027; MUID:99443731; PMID:10512747

A;Accession: JC7105

A;Molecule type: mRNA

A;Residues: 1-146 <CH>

A;Experimental source: venom gland

C;Superfamily: tetranectin; C-type lectin homology

C;Keywords: disulfide bond; platelet aggregation; venom

Query Match 11.7%; Score 121.5; DB 2; Length 146;
Best Local Similarity 23.3%; Pred. No. 0.0003;
Matches 37; Conservative 24; Mismatches 65; Indels 33; Gaps 7;

Qy 39 VVVALGILTVILMSLLYQRTLCGSKGFMCSQRCNLMWRNGSHCYFYSMEKRDWNS 98
Db 5 IFVSFGLLWVFLS-----LSGTGADCPGSSVYEGHCYKPFNEPKNWAD 48

Qy 99 SLKFC--ADKGSLLTFPDNQ-----VNLFOYVGEDFYWIGLRDI---DGRWEDGPA 149
Db 49 AERFCKLPKSHLVSFQSAEADFPVKLTLPRLKANLVMLGSLNIWHGCNQQWSDGARL 108

Qy 150 SILSILNSVQKCGTIHRCGLHAS-----SCEVALQWICE 184

Db 109 NYKDWQEO--SECLAFR--GVHTEMLNMDCSSTCSFVCK 143

RESULT 11

B42972

coagulation factor X activating enzyme (EC 3.4.24.-) light chain - Russell's viper

C;Species: Vipera russelli (Russell's viper)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997

C;Accession: B42972

R;Rakeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S.

J. Biol. Chem. 267, 14109-14117, 1992

A;Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A no

A;Reference number: A42972; MUID:92332516; PMID:1629211

A;Contents: V. r. siamensis

A;Accession: B42972

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-123 <TA>

A;Experimental source: venom

A;Note: sequence extracted from NCBI backbone (NCBIP:108408)

C;Superfamily: tetranectin; C-type lectin homology

C;Keywords: hydrolase; metalloproteinase; venom; zinc

F;4-121/Domain: C-type lectin homology <LCH>

F;4-15,32-121,98-113/Disulfide bonds: #status predicted

Query Match 11.1%; Score 115; DB 2; Length 123;
Best Local Similarity 33.8%; Pred. No. 0.001;
Matches 26; Conservative 12; Mismatches 29; Indels 10; Gaps 3;

Qy 75 CPNLMWRNGSHCYFYSMEKRDWNSLKFCAD--XGSHLLTFPDNQ-----VNLFOEYVGE 128
Db 4 CPSGWLSYEQHCYKGFNDLKNWTDAEKFTCEQKKGSHLVSLHSEEEFVVNLSLENLEY 63

Qy 129 DFYWGILRDIDGRWED 145

Db 64 PATWIGL-----GNWKD 76

RESULT 12

JC7134

agkisacutacin alpha chain precursor - sharp-nosed viper

N;Alternate names: fibrinogenolytic venom protein

C;Species: Agkistrodon acutus (sharp-nosed viper)

C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000

C;Accession: JC7134; PC7037

R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.

Biochem. Biophys. Res. Commun. 265, 530-535, 1999

A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic veno

A;Reference number: JC7134; MUID:20025379; PMID:10558903

A;Accession: JC7134

A;Molecule type: mRNA

A;Residues: 1-152 <CHE>

A;Cross-references: GB:AF176420

A;Experimental source: venom gland

A;Accession: PC7037

A;Molecule type: protein

A;Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>

C;Superfamily: tetranectin; C-type lectin homology

C;Keywords: disulfide bond; heterodimer; venom

F;1-23/Domain: signal sequence #status predicted <SIG>

F;124-152/Product: agkisacutacin alpha chain #status experimental <MAT>

Query Match 11.1%; Score 114.5; DB 2; Length 152;
Best Local Similarity 21.5%; Pred. No. 0.0014;
Matches 35; Conservative 22; Mismatches 73; Indels 33; Gaps 6;

Qy 39 VVVALGILTVILMSLLYQRTLCGSKGFMCSQRCNLMWRNGSHCYFYSMEKRDWNS 98
Db 5 IFVSFGLLWVFLS-----LSGTAAACSSGWSVYEGHCYKVPKQSKTWAD 48

Qy 99 SLKFCADK--GSHLLTFPDNQGNLFOYVGEDF-----YWIGLRDID-----GWRWED 145
Db 49 AESPCTKQVNGHLSVIESSEADFPVAHLIAQKTKSAKHVWIGLRAQNKQKQCSIEWSD 108

Qy 146 GPALSILSILNSVQKCGTIH--RCGLHASS---CEVALQWICE 184

Db 109 GSSISYENWIEESKKCLGVHETGFHKWENFYCEQQDPFVCE 151

RESULT 13

WVZP8

hepatic lectin homolog (BamHI-ORF8) - fowlpox virus (isolate HP-438 [Munich])

C;Species: fowlpox virus

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000

C;Accession: H29963

R;Tomley, F.; Birns, M.; Campbell, J.; Boursnell, M.

J. Gen. Virol. 69, 1025-1040, 1988

A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlp

A;Reference number: JT0442; MUID:88229622; PMID:2836548

A;Accession: H29963

A;Molecule type: DNA

A;Residues: 1-116 <TOM>

A;Cross-references: GB:D00295; NID:g221380; PIDN:BAA00203.1; PID:g221394

C;Superfamily: fowlpox virus hepatic lectin homolog; C-type lectin homology

C;Keywords: early protein

F;48-116/Domain: C-type lectin homology #status atypical <LEC>

Query Match 10.9%; Score 113; DB 1; Length 116;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:36:04 ; Search time 8 seconds
(without alignments)
1223.649 Million cell updates/sec

Title: US-09-811-367B-5

Perfect score: 1036

Sequence: 1 MADNSIYSTLELPAARVQD.....GLHASCEVALQWICEKVLIP 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 40997

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163.5	15.8	179	1	Q9mzk9 macaca mula
2	155	15.0	179	1	Q13241 homo sapien
3	155	15.0	179	1	Q9mz41 pan troglod
4	154	14.9	163	1	P14371 fowlpox vir
5	153.5	14.8	149	1	Q13241 homo sapien
6	148.5	14.3	133	1	RHCA_AGRKH
7	140.5	13.6	148	1	Q93427 agkistrodon
8	137	13.2	167	1	Q93427 croctalus du
9	132.5	12.8	117	1	P14370 fowlpox vir
10	131	12.6	157	1	P81509 croctalus ho
11	130	12.5	146	1	Q9Y999 agkistrodon
12	127.5	12.3	146	1	Q9Y192 agkistrodon
13	126	12.2	133	1	P23807 trimeresuru
14	124.5	12.0	123	1	P22029 bothrops ja
15	123.5	11.9	125	1	P81114 trimeresuru
16	113	10.9	162	1	P22030 bothrops ja
17	111.5	10.8	158	1	P07439 megabalanus
18	109.5	10.6	123	1	Q93426 croctalus du
19	109.5	10.6	155	1	P81113 trimeresuru
20	107.5	10.4	129	1	P82596 haliotis la
21	106.5	10.3	118	1	P81398 agkistrodon
22	103.5	10.0	131	1	P81116 trimeresuru
23	103.5	10.0	175	1	P81111 trimeresuru
24	103	9.9	174	1	Q06149 homo sapien
25	102	9.8	166	1	Q09049 mus musculu
26	101.5	9.8	133	1	P05451 homo sapien
27	100	9.7	135	1	P81017 echis carin
28	99.5	9.6	134	1	P21963 croctalus at
29	98	9.5	158	1	P81112 trimeresuru
30	98	9.5	165	1	Q95m11 pan troglod
31	97	9.4	158	1	P10758 rattus norv
32	96.5	9.3	123	1	O43908 homo sapien
33	96.5	9.3	152	1	P81996 echis carin
					P23806 trimeresuru

34	95	9.2	135	1	LECG_LACST	Q9psm4 lachesis st
35	95	9.2	166	1	LITB_HUMAN	P48304 homo sapien
36	94.5	9.1	175	1	PAP1_MOUSE	P35230 mus musculu
37	94	9.1	173	1	LIT2_MOUSE	Q08731 mus musculu
38	93	9.0	135	1	LECG_BITAR	Q9psn0 bitis ariet
39	92.5	8.9	158	1	LECG_TRIST	Q9ygp1 trimeresuru
40	92.5	8.9	174	1	PAP3_RAT	P42834 rattus norv
41	92	8.9	173	1	LECG_MEGRO	P17346 megabalanus
42	92	8.9	175	1	PAP1_RAT	P25031 rattus norv
43	91.5	8.8	175	1	PAP2_MOUSE	O09037 mus musculu
44	91	8.8	163	1	ANP_HEMAM	P05140 hemitripten
45	89.5	8.6	132	1	ABBA_TRIAB	P81115 trimeresuru

ALIGNMENTS

RESULT 1

CD94_MACMU						
ID	CD94_MACMU	STANDARD;	PRT;	179 AA.		
AC	Q9MZK9; Q9GK91; Q9MZK7; Q9MZK8;					
DT	28-FEB-2003 (Rel. 41, Created)					
DT	28-FEB-2003 (Rel. 41, Last sequence update)					
DT	10-OCT-2003 (Rel. 42, Last annotation update)					
DE	Natural killer cells antigen CD94 (NK cell receptor) (Killer cell					
DE	lectin-like receptor subfamily D, member 1).					
GN	KURDI OR CD94.					
OS	Macaca mulatta (Rhesus macaque).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;					
OC	Cercopitheidae; Macaca.					
OX	NCBI_TaxID=9544;					
LN	[1]					
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).					
RX	MEDLINE-20322487; PubMed-10866118;					
RA	LaBonte M.L., Levy D.B., Letvin N.L.;					
RT	"Characterization of rhesus monkey CD94/NKG2 family members and					
RT	identification of novel transmembrane-deleted forms of NKG2-A, B, C,					
RT	and D.";					
RL	Immunogenetics 51:496-499(2000).					
LN	[2]					
RP	SEQUENCE FROM N.A. (ISOFORM 1).					
RX	MEDLINE-21158386; PubMed-11261935;					
RA	Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;					
RT	"Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative					
RT	splicing of 5' exons in rhesus monkey decidua.";					
RL	Immunogenetics 53:69-73(2001).					
CC	-!- FUNCTION: Plays a role as a receptor for the recognition of MHC					
CC	class I HLA-E molecules by NK cells and some cytotoxic T-cells.					
CC	-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family					
CC	members.					
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein.					
CC	-!- ALTERNATIVE PRODUCTS:					
CC	Event=Alternative splicing; Named isoforms=3;					
CC	Name=1; Synonyms=CD94-A;					
CC	IsoId=Q9MZK9-1; Sequence=Displayed;					
CC	Name=2; Synonyms=CD94-B;					
CC	IsoId=Q9MZK9-2; Sequence=VSP_003055;					
CC	Name=3; Synonyms=CD94 alt;					
CC	IsoId=Q9MZK9-3; Sequence=VSP_003054;					
CC	-!- TISSUE SPECIFICITY: Natural killer cells.					
CC	-!- SIMILARITY: Contains 1 C-type lectin family domain.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
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CC	use by non-profit institutions as long as its content is in no way					
CC	modified and this statement is not removed. Usage by and for commercial					
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/					
CC	or send an email to licenses@isb-sib.ch).					
DR	EMBL; AF190931; AAF74527.1; -.					
DR	EMBL; AF190932; AAF74528.1; -.					

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DR EMBL; AF190933; AAF74529.1; -.
DR EMBL; AF294886; AAG34498.1; -.
DR HSP; P22897; IEGG.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00441; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; Polymorphism.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FTID=VSP_003054.
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 1 34 MAVFTTLWRLLISGTGLGICLSLMTGLILKNS -> MAA
FT FTID=VSP_003054.
FT VARSPLIC 105 105 L -> LQ (in isoform 2).
FT VARIANT 139 139 Y -> D.
FT SEQUENCE 179 AA; 20607 MW; 06212B44949527F07 CRC64;
Query Match 15.8%; Score 163.5; DB 1; Length 179;
Best Local Similarity 31.2%; Pred. No. 4.7e-09;
Matches 39; Conservative 19; Mismatches 58; Indels 9; Gaps 4;
QY 70 SQSRRCPNLRNGSHCYFMKRDWNSLKFCAQKSHLLTFPDNGVNLFOEYVCD 129
Db 56 SDCCSCHEKGYRCNYCFISEEKTWNESHFCASQKSLQLQNRDELDFMSS--SQH 113
QY 130 FYWIGL---RIDGWRWDGPAISLSILNSVVOQ---CGTHRCG-LHASSCEVALQWI 182
Db 114 FYWIGLSVEHTAWLWNGSALSQYLPFSPTFKPKNCIAYNSGNALDESCETKNRYI 173
QY 183 CEKVL 187
Db 174 CKQQL 178
RESULT 2
CD94 HUMAN
ID CD94 HUMAN STANDARD; PRT; 179 AA.
AC Q13241; Q43321; Q43773; Q9UBE3; Q9UEQ0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1) (KP43).
GN KLRF1 OR CD94.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RA Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
RA MEDLINE=96011848; PubMed=7589107;
RT "Molecular characterization of human CD94: a type II membrane
RT glycoprotein related to the C-type lectin superfamily.";
RL Eur. J. Immunol. 25:2433-2437(1995).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RX MEDLINE=98139529; PubMed=9472066;
RA Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,

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RA Lehrach H., Francis F., Lopez-Botet M.;
RT "Structure of the human CD94 C-Type lectin gene.";
RL Immunogenetics 47:305-309(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Biassoni R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA MEDLINE=98267245; PubMed=9601951;
RX Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,
RA Tohma S., Inoue T., Yamamoto K., Juji T.;
RT "A alternatively spliced form of the human CD94 gene.";
RL Immunogenetics 48:87-88(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
ALschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield A.S., Kraywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q13241-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q13241-2; Sequence=VSP_003053;
CC Name=3; Synonyms=CD94 alt;
CC IsoId=Q13241-3; Sequence=VSP_003052;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd94.htm".
CC -----
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CC -----
DR EMBL; U30610; AAC50291.1; -.
DR EMBL; Y14287; CAA74663.1; -.
DR EMBL; Y14288; CAA74663.1; JOINED.
DR EMBL; AJ000673; CAA04230.1; -.
DR EMBL; AJ000001; CAA03845.1; -.
DR EMBL; AB009597; BAA24450.1; -.
DR EMBL; AB010084; BAA24451.1; -.
DR EMBL; BC028009; AAB28009.1; -.
DR PDB; 1B6E; 15-JUN-99.

```


DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative C-type lectin protein FPV239 (BamHI-ORF8).
 GN FPV239.
 OS Fowlpox virus (FPV).
 OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Avipoxvirus.
 OC NCBI_TaxID=10261;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20193820; PubMed=10729156;
 RX MEDLINE=20193820; PubMed=10729156;
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
 RT "The genome of fowlpox virus";
 RL J. Virol. 74:3815-3831(2000).
 RL [2]
 RN SEQUENCE OF 1-116 FROM N.A.
 RP STRAIN=FP-9 / Isolate HP-438;
 RX MEDLINE=88229622; PubMed=2836548;
 RA Tomley F., Binns M., Campbell J., Boursnell M.E.G.;
 RT "Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
 of fowlpox virus";
 RL J. Gen. Virol. 69:1025-1040(1988).
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC EMBL; AF198100; AAF44583.1; --
 DR EMBL; D00295; BAA0203.1; --
 DR PIR; H29963; WMVZF8.
 DR HSSP; P05140; 2AFP.
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin c.1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 KW Hypothetical protein; Lectin.
 FT DOMAIN 48 159 C-TYPE LECTIN.
 SQ SEQUENCE 163 AA; 18635 MW; 5156DC892885532 CRC64;
 Query Match 14.9%; Score 154; DB 1; Length 163;
 Best Local Similarity 22.9%; Pred. No. 3.7e-08;
 Matches 38; Conservative 31; Mismatches 65; Indels 32; Gaps 5;
 QY 33 PCVSLVNMVALGLTLVILMS-----LLLYQRTLCGSGKFMCSQRCPLNLMRNGS 84
 Db 18 PGCS--IIIVLSVFVILSTRPVPPDIKILY-----CKEGWGVNKK 57
 QY 85 HCYPFEMKRDWNSLKFCAKGSHELLFPDQGNVLFQEVYGVDFYWGRLRID---GW 141
 Db 58 NCYFSEBKNNKSLAVERCKMDQGLTSSKEEFKFLRYKPGNHNWIKGVDFNGTW 117
 QY 142 RWEDGPALSLTSLNSVQKCTIHRGCHLHASSCEVALQWCEKVL 187
 Db 118 KLEDGSSYD-NIVPIKIGDCAYLSDRSIMSFCLPKPKWICRIIL 162
 RESULT 5
 CLE2 HUMAN
 ID CLE2 HUMAN STANDARD; PRT; 149 AA.
 AC Q92478; Q9BS74; Q9UQB4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE C-type lectin superfamily member 2 (Activation-induced C-type lectin).
 GN CLEC2 OR AICL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97190245; PubMed=9038101;
 RX Hamann J., Montgomery K.T., Lau S., Kucherlapati R., van Lier R.A.W.;
 RA "AICL, a new activation induced antigen encoded by the human NK gene
 complex";
 RT Immunogenetics 45:295-300(1997).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22388257; PubMed=10072769;
 RX Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.;
 RA "Selection of cDNAs encoding putative type II membrane proteins on the
 cell surface from a human full-length cDNA bank";
 RT Gene 228:161-167(1999).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Urinary bladder;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Sunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Expressed preferentially in lymphoid tissues,
 and in most hematopoietic cell types.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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 or send an email to license@isb-sib.ch).
 CC EMBL; X96719; CAA65480.1; --
 DR EMBL; AB015628; BAA76495.1; --
 DR EMBL; BC005254; AAO05254.1; --
 DR Genbank; HGNC:2053; CLECSF2.
 DR MIM; 603242; --
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0005530; F: lectin; TAS.
 DR GO; GO:0006960; P: antimicrobial humoral response (sensu Inver. .; TAS.
 DR InterPro; IPR001304; Lectin C.
 DR Pfam; PF00059; lectin c.1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 KW Glycoprotein; Transmembrane; Lectin; signal-anchor.
 FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 8 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 FT DOMAIN 26 149 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 42 145 C-TYPE LECTIN.
 FT DISULFID 46 BY SIMILARITY.

```
FT DISULFID 87 144 BY SIMILARITY.
FT DISULFID 123 136 BY SIMILARITY.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 M -> T (IN REF. 3).
FT CONFLICT 79 79 D -> H (IN REF. 1).
FT CONFLICT 107 107 D -> H (IN REF. 1).
SQ SEQUENCE 149 AA; 17307 MW; 0B4FED23424F6C55 CRC64;

Query Match 14.8%; Score 153.5; DB 1; Length 149;
Best Local Similarity 27.0%; Pred. No. 3.7e-08;
Matches 43; Conservative 27; Mismatches 68; Indels 21; Gaps 6;

QY 31 HRPVSVL-VVVALGLLTIVLSLLYQRTLCCKSGKFGMCSQCRPNLWNRNGSHCYF 89
Db 5 HKKCFIIVGLVITNTIITLV-----KLTDSQ-SLCPYDWIGFQNKCYF 49
QY 90 SMEKRDWNSLKFCADKGSLLTFPDNQGNVLFQEVYGVGDFYWGIRLDIDG--WRWEDGP 147
Db 50 SKEGDWNSKYNKSTQHADLTIIDNIEENFLRYKCSSDHWGLKMAKNRTGQWVDGA 109
QY 148 ALSLSI-LSNSVVQKCTHRCGLGHASSCEVALQWICEK 185
Db 110 TTFKSFGRGS--EGCAVLSDDGAATACRYTERKWKICK 146

RESULT 6
RCHA_AGRH STANDARD; PRT; 133 AA.
ID AC P81397;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 36, Last sequence update)
DE Rhodocetin alpha subunit.
OS Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Calloselasma.
OX NCBI_TaxID=8717;
RN [1]
RP SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RA Wang R., Kini R.M., Chung M.C.M.;
RT "Rhodocetin, a novel platelet aggregation inhibitor from the venom of Calloselasma rhodostoma (Malayan pit viper): synergistic and noncovalent interaction between its subunits.";
RL Biochemistry 38:7594-7593(1999).
CC -1- FUNCTION: A potent inhibitor of collagen-induced platelet aggregation. Individually, neither subunit inhibits platelet aggregation. Both subunits are essential.
CC -1- SUBUNIT: Heterodimer of one alpha and one beta subunit held together by noncovalent interactions rather than by intersubunit disulfide bridges.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=15955.90; MW ERR=1.44; METHOD=Electrospray.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23806; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
FT DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 127 BY SIMILARITY.
FT DISULFID 102 119 BY SIMILARITY.
SQ SEQUENCE 133 AA; 15962 MW; 386EAC519DFC674D CRC64;

Query Match 14.3%; Score 148.5; DB 1; Length 133;
Best Local Similarity 30.3%; Pred. No. 1e-07;
Matches 40; Conservative 27; Mismatches 46; Indels 19; Gaps 7;

QY 75 CPNLWNRNGSHCYFSEMEKRDWNSLKFCFCA--DKGSHLLTFPDNQGNVLFQEVYGVGDFY- 131
Db 2 CPDGSSTKSYCYRPFPEKKTWEAEARFCTEQEKAHLVSM-ENRLEAVFVDMVMENNFE 60
QY 132 -----WIGLR-DIDGWR-----WEDGPALSLSLNSVVQKCGTI-HRCGL--HASSCE 176
Db 61 NKIYRSWIGLTKENQORSNLEWSDGSSISYENLYEPYMEKCFMDHQSLPKWHTADCE 120
QY 177 VALQWICEKVLK 188
Db 121 EKNVFMCKFQLP 132

RESULT 7
CVXB_CRODU STANDARD; PRT; 148 AA.
ID AC O93437;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Convulxin beta precursor (CVX beta).
OS Crotalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
RC TISSUE=Venom gland;
RA Leduc M., Bon C.;
RT "Cloning of subunits of convulxin, a collagen-like platelet-aggregating protein from Crotalus durissus terrificus venom.";
RL Biochem. J. 333:389-393(1998).
CC -1- FUNCTION: Binds to the platelet and collagen receptor, glycoprotein VI (GPVI).
CC -1- SUBUNIT: Heterohexamer of three alpha chains and three beta chains; disulfide-linked.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
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CC -----
DR EMBL; Y16349; CAA76182.1; -.
DR HSP; P23807; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 148 CONVULXIN BETA.
FT DOMAIN 34 145 C-TYPE LECTIN.
FT DISULFID 26 26 INTERCHAIN (WITH C-158 IN ALPHA CHAIN) (POTENTIAL).
FT DISULFID 27 38 BY SIMILARITY.
FT DISULFID 55 144 BY SIMILARITY.
FT DISULFID 100 100 INTERCHAIN (WITH C-104 IN ALPHA CHAIN) (POTENTIAL).
FT DISULFID 121 136 BY SIMILARITY.
SQ SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;

Query Match 13.6%; Score 140.5; DB 1; Length 148;
Best Local Similarity 29.1%; Pred. No. 7.1e-07;
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CC -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,  

CC disulfide-linked.  

CC -!- SUBCELLULAR LOCATION: Secreted.  

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  

DR HSP; P23807; IIXX.  

DR InterPro; IPR002353; AntifreezeII.  

DR InterPro; IPR001304; Lectin_C.  

DR Pfam; PF00059; lectin_C; 1.  

DR PRINTS; PR00356; ANTIFREEZEII.  

DR SMART; SMO0034; CLECT; 1.  

DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.  

DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.  

KW Lectin.  

FT DOMAIN 1 121 C-TYPE LECTIN (LONG FORM).  

FT DISULFID 2 13 BY SIMILARITY.  

FT DISULFID 30 119 BY SIMILARITY.  

FT DISULFID 96 111 BY SIMILARITY.  

SQ SEQUENCE 123 AA; 14365 MW; D4CFBEEI219C9BI E CRC64;  

  

Query Match 12.0%; Score 124.5; DB 1; Length 123;  

Best Local Similarity 31.4%; Pred.No.2.2e-05;  

Matches 27; Conservative 15; Mismatches 31; Indels 13; Gaps 3;  

  

QY 75 CPNLWMENGSHCYFYFSMEKDWNSLKFCD--KGSHLLTFPDNQ-----VNI.FQEVVGE 128  

Db |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  

2 CPSWSSEYGHCYRVFNFPQNWDAEKFCCTQHKGSHLVFSQSSEADFFVQMTRPILNA 61  

  

QY 129 DFYWGIGLRDIDGW----RWEDGPAL 149  

Db |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  

62 NLWVGISNLS--WNQCSQMSDGTXL 85  

  

RESULT 15  

BOTB BOTJA  

ID BOTB BOTJA STANDARD; PRT; 125 AA.  

AC P22030;  

DT 01-AUG-1991 (Rel. 19, Created)  

DT 01-JUL-1993 (Rel. 26, last sequence update)  

DT 10-OCT-2003 (Rel. 42, last annotation update)  

DE Botrocetin, beta chain (Platelet coagglutinin).  

OS Bothrops jararaca (Jararaca).  

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  

OC Viperidae; Crotalinae; Bothrops.  

ON NCBI_TaxID=8724;  

RX [1]  

RN SEQUENCE-VENOM.  

RP RP  

RC TISSUE=Venom;  

RC MEDLINE=93157385; PubMed=8430107;  

RX Usumi Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,  

RA Titani K.;  

RA "Primary structure of two-chain botrocetin, a von Willebrand factor  

RT modulator purified from the venom of Bothrops jararaca.";  

RL Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).  

RN [2]  

RP SEQUENCE OF 1-40.  

RX TISSUE=Venom;  

RX MEDLINE=91129280; PubMed=1993206;  

RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,  

RA Fukui H., Sugimoto M., Ruggeri Z.M.;  

RT "Isolation and chemical characterization of two structurally and  

RT functionally distinct forms of botrocetin, the platelet coagglutinin,  

RT isolated from the venom of Bothrops jararaca.";  

RL Biochemistry 30:1957-1964(1991).  

RN [3]  

RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  

RX MEDLINE=22118144; PubMed=12121649;  

RA Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,  

RA Liddington R.C.;  

RT "Structural basis of von Willebrand factor activation by the snake  

RT toxin botrocetin";  

RL Structure 10:943-950(2002).  

CC -!- FUNCTION: Two-chain botrocetin forms an activated complex with

```

```
CC      vWF, and the complex then binds to platelet GPIb, resulting in
CC      platelet agglutination.
CC      -!- FUNCTION: There are two distinct forms of the von Willebrand
CC      factor-dependent platelet coagglutinin. The dimeric form is
CC      34-times more active than the one-chain botrocetin in promoting
CC      vWF binding to platelets.
CC      -!- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.
CC      Botrocetin and vWF form a soluble complex.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR      PIR; B47267; B47267.
DR      PDB; 1JK; 17-JUL-02.
DR      PDB; 1FVU; 14-FEB-01.
DR      InterPro; IPR002353; AntifreezeII.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; lectin_c; 1.
DR      PRINTS; PR00356; ANTIFREEZEII.
DR      SMART; SM00034; CLECT; 1.
DR      PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR      PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW      Lectin; 3D-structure.
FT      Disulfid 2 13
FT      Disulfid 30 121
FT      Disulfid 75 75
FT      Disulfid 98 113
SQ      SEQUENCE 125 AA; 15037 MW; 1ED2027ED817FCA0 CRC64;

Query Match      11.9%; Score 123.5; DB 1; Length 125;
Best Local Similarity 31.3%; Pred. NO. 2.8e-05;
Matches 26; Conservative 12; Mismatches 32; Indels 13; Gaps 4;

QY      75 CPNLWMRNGSHCYFSEMEKRDWNSSLKFCADK--GSHLLTFPDNQGVALFQEVYGE---- 128
DB      2 CPPDWSSYEGHCYRFKEMHMDDAEEFCTEQQTGAHLVSPQSKEADFVRSLTSEMLKG 61

QY      129 DFYIGLRIDIGW----RWEDG 146
DB      62 DVVWIGLSDV--WNKCFEWTIG 82
```

Search completed: August 10, 2004, 16:42:48
Job time : 9 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:39:05 ; Search time 32 Seconds
(without alignments)
1853.669 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSTLELPAAARVQD.....GLHASCEVALQWICEKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 396094

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	11	Q64335
2	838	80.9	188	11	O88713
3	178	17.2	181	4	Q9NZS1
4	175	16.9	179	11	O54708
5	175	16.9	179	11	O54707
6	173	16.7	165	11	Q9R007
7	171	16.5	165	6	Q9GLF4
8	165.5	16.0	164	11	Q8BL24
9	165	15.9	161	6	Q95JG4
10	161.5	15.8	185	6	Q9GLF3
11	161.5	15.6	179	6	Q8MHY8
12	160	15.4	154	4	Q8WUP7
13	160	15.4	159	6	Q8SPX0
14	159.5	15.4	188	4	Q9NY25
15	158.5	15.3	179	6	Q8MJ13
16	158.5	15.3	179	11	O35778

17	158	15.3	185	6	Q9MZJ6	Q9mzj6 macaca mula
18	157.5	15.2	132	11	Q8R4K5	Q8r4k5 rattus norv
19	157.5	15.2	180	12	Q9DLS8	Q9dlis8 rat cytoMeg
20	155.5	15.0	179	6	Q8MHY9	Q8mhy9 pongo pygma
21	155	15.0	178	11	Q91ZW9	Q91zw9 mus musculus
22	153	14.8	187	4	Q9UKQ0	Q9ukq0 homo sapien
23	152.5	14.7	179	6	Q8MJ14	Q8mj14 pongo pygma
24	150	14.5	146	13	Q8AYA4	Q8aya4 agkistrodon
25	149.5	14.4	168	11	Q9JKF2	Q9jkg2 mus musculus
26	148	14.3	173	4	Q9HD37	Q9hd37 homo sapien
27	146	14.1	146	13	Q8JIW1	Q8jiw1 agkistrodon
28	145	14.0	146	13	Q9IAM0	Q9iam0 agkistrodon
29	144	13.9	168	4	Q96FA7	Q96fa7 homo sapien
30	143	13.8	148	13	Q8AV98	Q8av98 trimeresuru
31	142	13.7	142	11	Q8CJ86	Q8cj86 mus musculus
32	142	13.7	158	11	Q8OZ35	Q8oz35 mus musculus
33	142	13.7	175	11	Q9JKF3	Q9jkg3 mus musculus
34	142	13.7	183	13	Q8OZS7	Q8ozs7 gallus gall
35	141	13.6	142	11	Q8BHK7	Q8bhk7 mus musculus
36	141	13.6	163	6	Q9GK90	Q9gk90 macaca mula
37	137	13.2	183	6	Q95J54	Q95j54 pan troglod
38	135.5	13.1	146	13	Q8JGT6	Q8jgt6 trimeresuru
39	135.5	13.1	158	13	Q8UVC6	Q8uvc6 agkistrodon
40	135.5	13.1	158	13	Q8AYA5	Q8aya5 agkistrodon
41	134.5	13.0	136	13	Q91841	Q91841 agkistrodon
42	134.5	13.0	146	13	Q7T045	Q7t045 vipera lebe
43	134	12.9	182	11	Q61972	Q61972 mus musculus
44	132.5	12.8	162	6	Q8MJH4	Q8mjh4 pongo pygma
45	132	12.7	164	11	Q9EP94	Q9ep94 mus musculus

ALIGNMENTS

RESULT 1

Q64335 ID Q64335 PRELIMINARY; PRT; 188 AA.
AC Q64335; DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MAFA protein.
GN MAFA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=Testis;
RA Bocek Jr P., Guthmann M.D., Pecht I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016176; PubMed=7568140;
RA Guthmann M.D., Tal M., Pecht I.;
RT "A secretion inhibitory signal transduction molecule on mast cells is
RT another C-type lectin."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL; X97191; CAA65829.1; JOINED.
DR EMBL; X97192; CAA65829.1; JOINED.
DR EMBL; X97193; CAA65829.1; JOINED.
DR EMBL; X97194; CAA65829.1; JOINED.
DR EMBL; X97195; CAA65829.1; JOINED.
DR EMBL; X97195; CAA65829.1; JOINED.
DR PIR; I59421; I59421.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT. 1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 188 AA; 21356 MW; 2CC8032D4D020B15 CRC64;

```
Query Match 100.0%; Score 1036; DB 11; Length 188;
Best Local Similarity 100.0%; Pred. No. 1e-102;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVVMVALGLLTVILMSLLLYQRTL 60
Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVVMVALGLLTVILMSLLLYQRTL 60

Qy 61 CCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKDWNSSLKFCADKGSLLHTFPDNOGVN 120
Db 61 CCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKDWNSSLKFCADKGSLLHTFPDNOGVN 120

Qy 121 LFOEYVGEDFWYIGLRIDGWRWEDGPALSLSILSNSVVOKGTTHRCGLHASSCEVALQ 180
Db 121 LFOEYVGEDFWYIGLRIDGWRWEDGPALSLSILSNSVVOKGTTHRCGLHASSCEVALQ 180

Qy 181 WICKVKLP 188
Db 181 WICKVKLP 188

RESULT 2
O88713 PRELIMINARY; PRT; 188 AA.
AC O88713
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-AUG-1999 (TREMBlrel. 11, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-
DE like receptor G1).
GN KLRG1 OR MAFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17 SCID;
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
[2]
RP SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvevTACfBr; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=11220622;
RA Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue
RT of MAFA.";
RL Immunogenetics 52:206-211(2001).
DR EMBL; AF097357; AAD03718.1; -
DR EMBL; AJ010751; CAA09342.1; -
DR EMBL; AF317727; AAK40082.1; -
DR MGB; MGI:1355294; Klrp1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; P:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EAL134F1 CRC64;
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Query Match 80.9%; Score 838; DB 11; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.6e-81;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
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```
Qy 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVVMVALGLLTVILMSLLLYQRTL 60
Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVVMVALGLLTVILMSLLLYQRTL 60

Qy 61 CCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKDWNSSLKFCADKGSLLHTFPDNOGVN 120
Db 61 CCGSKDGTCSHCPCILWTRNGSHCYFYSMEKDWNSSLKFCADKGSLLHTFPDNOGVK 120

Qy 121 LFOEYVGEDFWYIGLRIDGWRWEDGPALSLSILSNSVVOKGTTHRCGLHASSCEVALQ 180
Db 121 LFGYLGQDFYWIGLRIDGWRWEGGPALSRLITNSLTQCGAIHRNGLOASSCEVALQ 180

Qy 181 WICKVKLP 187
Db 181 WICKVKLP 187

RESULT 3
Q9NZS1 PRELIMINARY; PRT; 181 AA.
AC Q9NZS1
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Lectin-like receptor F1, splice variant 1 KLRF1-sl.
GN KLRF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KLRF1, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
DR EMBL; AF175207; AAF37805.1; -
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CAB1E551 CRC64;
```

```
Query Match 17.2%; Score 178; DB 4; Length 181;
Best Local Similarity 25.0%; Pred. No. 6.2e-11;
Matches 51; Conservative 32; Mismatches 77; Indels 44; Gaps 9;
```

```
Qy 1 MADNSIYSTLELPAAPRVQ--DDSRMKV---AVLHRPCVSYLVVMVAL-----GLTVILM 51
Db 1 MDDEERYMTLVNQSKRSSAQTSQITPKDYSVTLH---WYKILGISGTWNGILTALI 56

Qy 52 SLLLYQRTLCCGSKGFMCSCQRCPNLWMRNGSHCYFYSMEKDWNSSLKFCADKGSLL 111
Db 57 SLLIL-----LVLQSEWLKYGKCYFWSNEMKGSWSDSYVYCLERKSHLL 100

Qy 112 TFPDNOGVNLFQEVGE--DFYWIGLRIDID--GWRWEDGPALSLSIL-----SNSVYVQ 160
Db 101 IHHQLEMAFIQKRLQNLQVYVYVIGLNTSLKMTWTWVDGSPIDSKIPKIPKPAKENS--- 157

Qy 161 KGTIHRGCLHASSCEVALQWICE 184
Db 158 -CAAIKESKIFSETCSSVFKWICQ 180
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RESULT 4
O54708
```



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FT NON TER 161 161
SQ SEQUENCE 161 AA; 18648 MW; 24F9AA4A19EAFB7 CRC64;

Query Match
Best Local Similarity 15.9%; Score 165; DB 6; Length 161;
Matches 38; Conservative 19; Mismatches 56; Indels 8; Gaps 4;

QY 75 CPNLMWRNGSHCYFSEMEKEDWNSLKFCADKGSLLITFPDQGVNLFQBYVGED--FYW 132
Db 41 CPNLMWRNGSHCYFSEMEKEDWNSLKFCADKGSLLITFPDQGVNLFQBYVGED--FYW 132
QY 133 IGLR-DIDG---WRWEDGPALES---LSILSNSVVGKGTTHRCGLHASSCEVALQWICEKV 186
Db 101 IGLNFTLSGSKRWINGSFLNSILPFGDAKEDCCVYISKTCISIDYCAAKRWICQKE 160
QY 187 L 187
Db 161 L 161

RESULT 10
Q9GLF3 PRELIMINARY; PRT; 185 AA.
AC Q9GLF3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myeloid DAPI2-associating lectin long form.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=21308528; PubMed=11414735;
RA Yim D., Jie H.B., Sotiriadis J., Kim Y.S., Kim Y.B.;
RT "Molecular cloning and expression pattern of porcine myeloid DAPI2-
RT associating lectin-1";
RL Cell. Immunol. 209:42-48(2001).
DR EMBL; AF285450; AAG29428.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 185 AA; 20835 MW; DA6EC0AF58BC95CE CRC64;

Query Match
Best Local Similarity 15.8%; Score 164; DB 6; Length 185;
Matches 49; Conservative 22; Mismatches 72; Indels 38; Gaps 5;

QY 40 MVALGLTLVIL----MSLLIYQRTLCGSGKGFMCSCQR----- 74
Db 5 MIISGLIVVVKLVGVMTFFLLYPQFGEHNVFSFSTPRTGTVQIFGSGNSFTTSEF 64
QY 75 ---CPNLMWRNGSHCYFSEMEKEDWNSLKFCADKGSLLITFPDQGVNLFQBYVGEDFY 131
Db 65 GTVCPGTGDPHQRCFPFLSTSENSWNNMNFCKGKSTLAIVNTPEKLFQNISGAEKY 124
QY 132 WIGURDIDG---WRWEDGPALESILSNSVVGKGTTHRCGL-----HASSCEVALQWICE 184
Db 125 FGLLYQPAEKMRWINNSVFNFSVISHNFNCVTI---GLTKTFDAASCDVNYRSICE 181
QY 185 K 185
Db 182 K 182

RESULT 11
Q8MHY8 PRELIMINARY; PRT; 179 AA.
ID Q8MHY8

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AC Q8MHY8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Natural killer cell receptor.
GN POPY-CD94.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
NCBI_TaxID=9600;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHG-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470381; AAM78481.1; -.
DR EMBL; AF470382; AAM78482.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20550 MW; 6752CB8F182CFD73 CRC64;

Query Match
Best Local Similarity 15.8%; Score 161.5; DB 6; Length 179;
Matches 48; Conservative 25; Mismatches 84; Indels 19; Gaps 7;

QY 24 WKYKAVLHPRCVSYLVWVALGILLTVILMSLLYQRTLCG-----SKGFMCSCSCPNL 78
Db 10 WLISGTLGIICLS--LMATLIGLLKNSFTKLSTIEPAFTPGDIELOKD---SPCCSCQEK 64
QY 79 WMRNGSHCYFSEMEKEDWNSLKFCADKGSLLITFPDQGVNLFQBYVGEDFYWIGL--- 135
Db 65 WVGRCNCYFISSEQKTWNEHLCASQKSSLLQLQNTDDELDPMS--SQQFWIGLSYS 122
QY 136 RIDGWRWEDGPALES---LSILSNSVVGKGTTHRCG-LHASSCEVALQWICEKV 187
Db 123 EEHTAWLWENGSAISQYLFLETFETFPKNCIAYPNPNALDESCDKNRYICKQOL 178

RESULT 12
Q8WUP7 PRELIMINARY; PRT; 154 AA.
ID Q8WUP7
AC Q8WUP7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to lectin-like NK cell receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX TISSUE=Testis;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019883; AAH19883.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.

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```
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20566 MW; 6752CB8F0F9A2609 CRC64;

Query Match 15.3%; Score 158.5; DB 6; Length 179;
Best Local Similarity 26.7%; Pred. No. 7.5e-09;
Matches 47; Conservative 26; Mismatches 84; Indels 19; Gaps 7;

Qy 24 WKVAVLHRPCVSYLVVVALGLLTIVILMSLLLYQRTILCCG-----SKGFMCSCQCSRCPNL 78
   | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 10 WLISGTLGIICLS--LMATLGIILKNSFTKLSIEPAFTPGPDIELQKD---SDCCSCQEK 64

Qy 79 WMRNGSHCYFESMEKRDWNSSLKFCADKSGHLLTFPDNQGVNLFQEVYVGEDFYWIGL--- 135
   | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 65 WVGRCNCYFISSEQKTWNEsrHLCAQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYS 122

Qy 136 RDIDGWZWDGPALS--LSILSNSVVKCGTIHRCG-LHASSCEVALQWICEKVL 187
   : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 123 EEHTAWLWENGSSLSQYLPLFETFPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
```

Search completed: August 10, 2004, 16:44:03
Job time : 32 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:35:35 ; Search time 47.5 Seconds

(without alignments)
1118.293 Million cell updates/sec

Title: US-09-811-367B-5

Perfect score: 1036

Sequence: 1 MADNSYISTLELPAARVQD.....GLHASCEVALQWICEKVL P 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1082526

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2	AAR77033 Mammalian
2	1036	100.0	188	2	AAW89277 Rat mast
3	1036	100.0	188	4	AAE11761 Rat mast
4	838	80.9	188	4	AAE11760 Mouse mas
5	651	62.8	114	2	AAE11760 Mouse mas
6	207.5	20.0	99	2	AAW88267 Human MAF
7	170	16.4	165	4	AAU00673 Human INT
8	170	16.4	165	6	ABO32541 Secreted
9	164.5	15.9	182	4	AAU19660 Human nov
10	164.5	15.9	182	5	ABP47880 Human pol
11	164.5	15.9	182	7	ADC10842 Human ext
12	163.5	15.8	142	4	AAW80296 Human pro
13	163.5	15.8	142	6	ABG72616 Human Cyt
14	163.5	15.8	160	4	AAW80302 Human pro
15	163	15.7	145	4	AAU00675 Human INT
16	163	15.7	145	6	ABO32547 Secreted
17	161	15.5	181	2	AAW27288 Human G52
18	161	15.5	181	7	ADC38664 Human sec
19	160	15.4	162	2	AAW27446 Human SDC
20	159.5	15.4	188	4	AAW78675 Human pro
21	159.5	15.4	188	4	AAU00671 Human INT
22	159.5	15.4	188	6	ABO32533 Secreted
23	158.5	15.3	167	2	AAW63022 Mouse dec
24	156.5	15.1	149	2	AAW36957 Protein e
25	155	15.0	179	2	AAW64791 Human Kp4

ALIGNMENTS

RESULT 1

AAAR77033
ID AAR77033 standard; protein; 188 AA.

XX AAR77033;

XX DT 01-FEB-1996 (first entry)

XX DE Mammalian mast cell function-associated antigen (MAFA).

XX KW Mast cell function-associated antigen; MAFA; soluble; ligand;

KW identification; screening; inflammation; inflammatory; allergy; allergic;

KW prevention.

XX OS Rattus rattus.

XX WO9527734-A1.

XX PD 19-OCT-1995.

XX PF 06-APR-1995; 95WO-US004258.

XX PR 08-APR-1994; 94IL-00109257.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI (RYCU//) RYCUS A.

XX PI Pecht I, Guthmann MD, Tal M;

XX DR WPI; 1995-366356/47.

XX DR N-PSDB; AAT01471.

XX PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -
useful for screening for ligands of MAFA which are useful for prevention
of inflammatory and allergic reactions.

XX PS Claim 12; Page 37; 54pp; English.

XX CC A soluble form of mast cell function-associated antigen (MAFA) can be
produced by recombinant techniques for use in the ligand- screening
assay. The ligands that are identified may be used alone or in
combination with the MAFA to prevent inflammatory and allergic reactions

SQ Sequence 188 AA;

Query Match

Best Local Similarity 100.0%; Score 1036; DB 2; Length 188;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRCPCVSYLVVMVALGLLTVILMSLLLYQRTL 60
 Db 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRCPCVSYLVVMVALGLLTVILMSLLLYQRTL 60
 QY 61 CCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKRDWNSLKFCDKAGSHLLTFFDNQGVN 120
 Db 61 CCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKRDWNSLKFCDKAGSHLLTFFDNQGVN 120
 QY 121 LFOEYVGEDFYWIGLRDIDGWRWEDGPAISLSILSNSVQKCGTHRCGLHASSCEVALQ 180
 Db 121 LFOEYVGEDFYWIGLRDIDGWRWEDGPAISLSILSNSVQKCGTHRCGLHASSCEVALQ 180
 QY 181 WICEKVLP 188
 Db 181 WICEKVLP 188

RESULT 2
 AAW88277
 ID AAW88277 standard; protein; 188 AA.
 AC AAW88277;
 XX 29-MAR-1999 (first entry)
 DT Rat mast cell function-associated antigen (MAFA).
 DE Mast cell function-associated antigen; MAFA; splice variant; rat;
 KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
 XX Rattus sp.
 FH Key Location/Qualifiers
 FT Modified-site 82..84
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 97..99
 FT /note= "Asn is N-glycosylated"
 XX WO9854209-A2.
 XX 03-DEC-1998.
 XX 29-MAY-1998; 98WO-GB001572.
 XX 31-MAY-1997; 97GB-00011148.
 XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
 XX WPI; 1999-059806/05.
 XX N-PSDB; AAW84222.
 XX New polypeptide having a sequence corresponding to human mast cell
 PT function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.
 XX Disclosure; Fig 4; 44pp; English.
 XX This is the amino acid sequence of rat mast cell function-associated
 CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and
 CC basophils. The invention relates to cloning of the human MAFA molecule
 CC (see AAW88265) and to the discovery of splice variants (see AAW88266-67)
 CC of human MAFA that are not found in rat. Polypeptides and synthetic
 CC peptides (see AAW88258-64) based on human MAFA and human truncated MAFA,
 CC and polynucleotides encoding them, can be used in methods for the
 CC treatment of inflammatory and allergic diseases (e.g. rheumatoid
 CC arthritis and asthma), and tumour growth
 XX Sequence 188 AA;
 SQ

Query Match 100.0%; Score 1036; DB 2; Length 188;
 Best Local Similarity 100.0%; Pred. No. 1.8e-96;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRCPCVSYLVVMVALGLLTVILMSLLLYQRTL 60
 Db 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRCPCVSYLVVMVALGLLTVILMSLLLYQRTL 60
 QY 61 CCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKRDWNSLKFCDKAGSHLLTFFDNQGVN 120
 Db 61 CCGSGKGFMCSCQRCPNLWMRNGSHCYFYSMEKRDWNSLKFCDKAGSHLLTFFDNQGVN 120
 QY 121 LFOEYVGEDFYWIGLRDIDGWRWEDGPAISLSILSNSVQKCGTHRCGLHASSCEVALQ 180
 Db 121 LFOEYVGEDFYWIGLRDIDGWRWEDGPAISLSILSNSVQKCGTHRCGLHASSCEVALQ 180
 QY 181 WICEKVLP 188
 Db 181 WICEKVLP 188

RESULT 3
 AAE11761
 ID AAE11761 standard; protein; 188 AA.
 AC AAE11761;
 XX 18-DEC-2001 (first entry)
 DT Rat mast cell function-associated antigen (MAFA) protein.
 DE Rat; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 XX Rattus norvegicus.
 OS WO200170805-A2.
 XX 27-SEP-2001.
 XX 16-MAR-2001; 2001WO-US008596.
 XX 17-MAR-2000; 2000US-0190716P.
 XX (GEMI-) GEMINI SCI INC.
 XX Takahashi N, Mikayama T;
 XX WPI; 2001-611482/70.
 XX N-PSDB; AAD18736.
 XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX Example 1; Page 19; 49pp; English.
 XX The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is rat MAFA protein

```

XX SQ Sequence 188 AA;
Query Match 100.0%; Score 1036; DB 4; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.8e-96;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVODDSRWKVKAVLHRCPCVSYLVNVALGLLTVILMSLLLYQRTL 60
DB 1 MADNSIYSTLELPAAPRVODDSRWKVKAVLHRCPCVSYLVNVALGLLTVILMSLLLYQRTL 60

QY 61 CCGSGKGFMCQSCRCPNLWNRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTTPFDNOGVN 120
DB 61 CCGSGKGFMCQSCRCPNLWNRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTTPFDNOGVN 120

QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLILSLSNSVVKCGTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLILSLSNSVVKCGTHRCGLHASSCEVALQ 180

QY 181 WICEKVLP 188
DB 181 WICEKVLP 188

RESULT 4
ID AAE11760 standard; protein; 188 AA.
XX AAE11760;
XX AAE11760;
DT 18-DEC-2001 (first entry)
DE Mouse mast cell function associated antigen (MAFA) protein.
XX Mouse; pharmaceutical composition; mast cell function associated antigen;
XX MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
XX immunosuppressive; cytostatic.
XX Mus sp.
XX Key Location/Qualifiers
FH Domain 64..188
FT /note="Extracellular domain"
XX
XX WO200170805-A2.
XX
XX 27-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US008596.
XX
XX 17-MAR-2000; 2000US-0190716P.
XX
XX (GEMI-) GEMINI SCI INC.
XX
XX Takahashi N, Mikayama T;
XX
XX WPI; 2001-611482/70.
XX
XX N-PSDB; AAD18735.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
XX activity of natural killer cell or T-cell, comprises an agent that binds
XX to mast cell function-associated antigen ligand on target cell.
XX
XX Example 1; Page 19; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
XX an agent which specifically binds to a mast cell function associated
XX antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
XX killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
XX ligand and a pharmaceutically acceptable excipient. The invention is
XX useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
XX binding to a ligand on a target cell, by contacting the pharmaceutical
XX composition in vitro, ex vivo or in vivo by administering the composition
XX
XX to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
XX an amount sufficient to inhibit cell surface MAFA binding to the ligand
XX on the target cell. The agent or the composition is useful for treating a
XX tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
XX T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
XX tumour cell. The invention is also useful for inhibiting an activity of
XX NK cell or a T-cell. The present sequence is mouse MAFA protein
XX
XX SQ Sequence 188 AA;
Query Match 80.9%; Score 838; DB 4; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.9e-76;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVODDSRWKVKAVLHRCPCVSYLVNVALGLLTVILMSLLLYQRTL 60
DB 1 MADSSIYSTLELPEAQVQDESRLKAVLHRLPHLSRFAMVALGLLTVILMSLLMYQRL 60

QY 61 CCGSGKGFMCQSCRCPNLWNRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTTPFDNOGVN 120
DB 61 CCGSKDSTCSHCPCFILTWRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTTPFDNOGVK 120

QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLILSLSNSVVKCGTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGEDFYWIGLRIDGWRWEGGPALSLRLTNSLORCAIHRNGLQASCEVALQ 180

QY 181 WICEKVLP 187
DB 181 WICKKVL 187

RESULT 5
ID AAR77472 standard; protein; 114 AA.
XX AAR77472
XX AAR77472;
XX AAR77472;
DT 01-FEB-1996 (first entry)
DE Partial sequence of mast cell function-associated antigen (MAFA).
XX Mast cell function-associated antigen; MAFA; soluble; ligand;
XX identification; screening; inflammation; inflammatory; allergy; allergic;
XX prevention.
XX Rattus rattus.
XX
XX WO9527734-A1.
XX
XX 19-OCT-1995.
XX
XX 06-APR-1995; 95WO-US004258.
XX
XX 08-APR-1994; 94IL-00109257.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX (RYCU/) RYCUS A.
XX
XX Pecht I, Guthmann MD, Tal M;
XX
XX WPI; 1995-366356/47.
XX
XX N-PSDB; AAT01471.
XX
XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
XX useful for screening for ligands of MAFA which are useful for prevention
XX of inflammatory and allergic reactions.
XX
XX Disclosure; Page 38; 54pp; English.
XX
XX A soluble form of mast cell function-associated antigen (MAFA) can be
XX produced by recombinant techniques for use in the ligand- screening
XX assay. The ligands that are identified may be used alone or in
XX combination with the MAFA to prevent inflammatory and allergic reactions

```

XX SQ Sequence 114 AA; Query Match 62.8%; Score 651; DB 2; Length 114; Best Local Similarity 100.0%; Pred. No. 8.1e-58; Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 CPNLMWRNGSHCYFFSMKRDWNSLKFCADKSGHLLTFPDNQGYNLFQEVVGEDFYWIG 134
DB 1 CPNLMWRNGSHCYFFSMKRDWNSLKFCADKSGHLLTFPDNQGYNLFQEVVGEDFYWIG 60

QY 135 LRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQWICEKVL 188
DB 61 LRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQWICEKVL 114

RESULT 6
AAW88267
ID AAW88267 standard; protein; 99 AA.
XX AC AAW88267;
XX DT 29-MAR-1999 (first entry)
XX DE Human MAFA splice variant huMAFA(E3/4-).
XX KW Mast cell function-associated antigen; MAFA; huMAFA(E3/4-);
XX KW splice variant; human; inflammation; allergy; asthma;
XX KW rheumatoid arthritis; tumour; therapy.
XX OS Homo sapiens.
XX PN WO9854209-A2.
XX PD 03-DEC-1998.
XX PF 29-MAY-1998; 98WO-GB001572.
XX PR 31-MAY-1997; 97GB-00011148.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX DR WPI; 1999-059806/05.
XX DR N-PSDB; AAW84200.
XX PT New polypeptide having a sequence corresponding to human mast cell
PT function-associated antigen - useful in forming and manufacturing
PT pharmaceutical compositions in the treatment of inflammatory and allergic
PT diseases, and tumour growth.
XX PS Disclosure; Fig 3; 44pp; English.
XX CC This is the amino acid sequence of human mast cell function- associated
CC antigen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-
CC like domain of human MAFA (see AAW88265) but retains the intracellular
CC and transmembrane domains as well as the extracellular C-terminal tail.
CC Truncated MAFA polypeptides including huMAFA(E3/4-), and polynucleotides
CC encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-
CC 72), can be used in compositions for the treatment of
CC inflammatory and allergic diseases (e.g. rheumatoid arthritis and
CC asthma), or tumour growth
XX SQ Sequence 99 AA;

Query Match 20.0%; Score 207.5; DB 2; Length 99;
Best Local Similarity 29.6%; Pred. No. 4.7e-13;
Matches 55; Conservative 12; Mismatches 30; Indels 89; Gaps 1;

QY 1 MADNSTYSTLELPAPRVODDSRWKVKAVLHRCVSLVMVALGLITVILMSLLLYQRTL 60
DB 1 MTDSTVYSMLLELPTATQANDYGPQKSSSRPSCSLVALALGLTAVLLSVLLYQWL 60

QY 61 CCGSGFMCWCSQSRCPNLMWRNGSHCYFFSMKRDWNSLKFCADKSGHLLTFPDNQGYN 120
DB 61 CCG----- 63

QY 121 LFQBYVGEDFYWIGLRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQ 180
DB 64 -----ISSNPFVOTCGAITKNGLOASSCEVPLH 91

QY 181 WICEKV 186
DB 92 WVCKKV 97

RESULT 7
AAU00673
ID AAU00673 standard; protein; 165 AA.
XX AC AAU00673;
XX DT 07-SEP-2001 (first entry)
XX DE Human INTERCEPT 289 form 2a polypeptide.
XX KW Human; INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain;
KW skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;
KW bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;
KW anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease;
KW malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
KW attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
KW hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
KW muscular dystrophy; immuno-competence; vertebrae; blood; serum; lung.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Domain 7..27
FT Domain /note= "Transmembrane domain"
FT Domain 28..165
FT Domain /note= "Extracellular domain"
XX WO200129088-A1.
XX PD 26-APR-2001.
XX PF 23-JUN-2000; 2000WO-US017386.
XX PR 19-OCT-1999; 99US-00420707.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Mackay CR, Myers PS, Kirst SJ, Fraser CC, Leiby KH;
XX DR WPI; 2001-308477/32.
XX DR N-PSDB; AAS00663.
XX PT New isolated nucleic acid molecule for diagnosis, prevention, and therapy
PT of human and other animal disorder, or as modulating agent for regulating
PT cellular processes.
XX Claim 8; Fig 2H-2I; 263pp; English.
XX CC The sequence represents human INTERCEPT 289 form 2a polypeptide. This
CC protein and similar others exhibit the ability to affect growth,
CC proliferation, survival, differentiation, activity, morphology, or
CC movement/migration of, e.g. T cells and cells of the heart, liver,
CC pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph
CC node, peripheral blood leukocyte, bone marrow or thymus tissue. They can
CC be used as modulating agents for regulating cellular processes, thus, the
CC proteins and their associated nucleic acids can be used to prognosticate,
CC prevent, diagnose, or treat disorders associated with physiological
CC processes. These disorders include abnormal blood coagulation, asthma,
CC anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery

CC disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis,
 CC meningitis, attention deficit disorder, Crohn's disease, gastroenteritis,
 CC goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary
 CC embolism and muscular dystrophy. Antibodies to disorders such as these
 CC can be made by providing a polypeptide of the invention to an immuno-
 CC competent vertebrate and harvesting blood or serum from the vertebrate
 XX
 XX Sequence 165 AA;
 Query Match 16.4%; Score 170; DB 4; Length 165;
 Best Local Similarity 27.3%; Pred. No. 5.5e-09;
 Matches 44; Conservative 31; Mismatches 68; Indels 18; Gaps 5;
 QY 40 MVALGLTLVIL-----MSLLLYQRTLCCKSGKFMCSQC--SRCPNLMWRNGSHCYFFSM 91
 Db 5 MIISGLIVLVVVKVGMVTLFLLYFPQIFNKNSDGTTRSYGTVCPKDWFFQARCFELST 64
 QY 92 EKRDWNSSLKFCADKGSLLTFFPDNQGNVLFQYVGEDFYWIGL---RDIDGWRWEDGPA 148
 Db 65 SESSWNESEDFCKGSGTLAIVNTPKLFQDITDAEKYFGLIYHREKRWWINNSV 124
 QY 149 LSLILNSVVKCGTTHRCGL-----HASSCEVALOWICEK 185
 Db 125 FNGNVNQNFNCATI---GLTKTFDAASCDISYRICEK 162
 RESULT 8
 ABO32541
 ID ABO32541 standard; protein; 165 AA.
 XX
 AC ABO32541;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE
 DE Secreted polypeptide-related protein #24.
 XX
 KW Human; TANGO; INTERCEPT; secreted polypeptide; immune disorder;
 KW hormonal disorder; proliferative disorder; cancer; thyroid disorder;
 KW diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disease;
 KW myocardial infarction; congestive heart disease; blood platelet disorder;
 KW thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
 XX
 OS Homo sapiens.
 XX
 XX US2003022279-A1.
 XX
 XX 30-JAN-2003.
 XX
 XX 12-JAN-2001; 2001US-00759130.
 XX
 XX 14-JUN-1999; 99US-00333159.
 XX 29-JUN-1999; 99US-00342364.
 XX 10-SEP-1999; 99US-00393996.
 XX 19-OCT-1999; 99US-00420707.
 XX 07-JAN-2000; 2000US-00479249.
 XX 27-APR-2000; 2000US-00559497.
 XX 24-MAY-2000; 2000US-00578063.
 XX 16-JUN-2000; 2000US-00596194.
 XX 23-JUN-2000; 2000US-00602871.
 XX 30-JUN-2000; 2000US-00608452.
 XX
 XX (FRASER C C.
 XX (BARNES T M.
 XX (SHARP J D.
 XX (KIRST S J.
 XX (MYERS P S.
 XX (LEIBY K R.
 XX (HOLTZMAN D A.
 XX (MCCARTHY S A.
 XX (WRIGHT N.
 XX (MACKAY C R.
 XX (GOOD/ GOODEARL A D J.

XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
 XX WPI; 2003-456290/43.
 DR N-PSDB; ACD66723, ACD66724.
 XX
 PT New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
 TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
 PT treating disorders such as cancer, diabetes or atherosclerosis, and in
 PT forensic biology.
 XX
 PS Claim 9; Fig 11H-11K; 482pp; English.
 XX
 CC The invention relates to secreted polypeptide-related proteins and
 CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
 CC nucleic acids, proteins and antibodies specific to the proteins are
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
 CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
 CC prophylactic and therapeutic methods. The sequences are used in
 CC diagnosing, preventing or treating proliferative disorders (e.g.
 CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
 CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
 CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
 CC disorders (e.g. myocardial infarction or congestive heart disease), blood
 CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
 CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
 CC acids may also be used in chromosome mapping, tissue typing and forensic
 CC biology, and as surrogate markers. This sequence represents a secreted
 CC polypeptide-related protein of the invention. Note: The sequence data for
 CC this patent was obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 165 AA;
 Query Match 16.4%; Score 170; DB 6; Length 165;
 Best Local Similarity 27.3%; Pred. No. 5.5e-09;
 Matches 44; Conservative 31; Mismatches 68; Indels 18; Gaps 5;
 QY 40 MVALGLTLVIL-----MSLLLYQRTLCCKSGKFMCSQC--SRCPNLMWRNGSHCYFFSM 91
 Db 5 MIISGLIVLVVVKVGMVTLFLLYFPQIFNKNSDGTTRSYGTVCPKDWFFQARCFELST 64
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 DT 04-DEC-2001 (first entry)
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 KW Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV;
 KW antianemic; antirheumatic; antisclerotic; cardiant; vascular;
 KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;
 KW antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
 KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
 KW cancers; hyperproliferative disorder; breast neoplasm; melanoma;
 KW Sezary syndrome; Gaucher's disease; neurological diseases;
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 KW cardiac arrest; tachycardia; angina; infection; corneal infections;
 KW wound healing; immunogen; gene therapy; antisense; food additive.
 XX

(ABP47846-ABP48110) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic disorders e.g. autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocId=999909764870

RESULT 11
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ID ADC10842 standard; protein; 182 AA.
ADC10842

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Extracellular matrix protein; cytostatic; antibacterial; virucide;
neuroprotective; gynaecological; gastrointestinal-Gen; cardiant;
cardiovascular-Gen; nephrologic; antiinflammatory; muscular-Gen;
respiratory-Gen; immunosuppressive; cerebroprotective; vasotropic;
neurotic; antiallergic; cancer; bacterial infection; viral infection;
neural disorder; immune system disorder; blood disorder;
muscular disorder; reproductive disorder; gastrointestinal disorder;
pulmonary disorder; cardiovascular disorder; renal disorder;
inflammatory disorder; proliferative disorder; Human.

OS Homo sapiens.

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US2003059875-A1.

27-MAR-2003

19-APR-2002: 2002US-00125540-XX PF

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	838	80.9	188	9	US-09-811-367B-3	Sequence 3, Appli
3	170	16.4	165	10	US-09-759-130B-98	Sequence 98, Appl
4	170	16.4	165	16	US-10-741-790-98	Sequence 98, Appl
5	167.5	16.2	161	10	US-09-766-511B-55	Sequence 55, Appl
6	164.5	15.9	182	9	US-09-764-870-310	Sequence 310, App
7	164.5	15.9	182	14	US-10-125-540-310	Sequence 310, App
8	163	15.7	145	10	US-09-759-130B-108	Sequence 108, App
9	163	15.7	145	16	US-10-741-790-108	Sequence 108, App
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11	160	15.4	162	14	US-10-270-470-2	Sequence 2, Appli
12	159.5	15.4	188	10	US-09-759-130B-83	Sequence 83, Appl
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18	154	14.9	138	16	US-10-741-790-100	Sequence 100, App
19	154	14.9	162	10	US-09-759-130B-85	Sequence 85, Appl
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21	153.5	14.8	140	9	US-09-764-870-340	Sequence 340, App
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31	153	14.8	162	12	US-10-239-656-90	Sequence 90, Appl
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33	153	14.8	187	16	US-10-741-790-86	Sequence 86, Appl
34	153	14.8	187	16	US-10-775-640-12	Sequence 12, Appl
35	147.5	14.2	94	9	US-09-764-870-466	Sequence 466, App
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38	146	14.1	146	12	US-10-296-115-1275	Sequence 1275, Ap
39	145	14.0	117	10	US-09-759-130B-110	Sequence 110, App
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41	144.5	13.9	119	9	US-09-764-870-302	Sequence 302, App
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45	142	13.7	124	12	US-10-072-012-836	Sequence 836, App

ALIGNMENTS

RESULT 1

US-09-811-367B-5

; Sequence 5, Application US/09811367B

; Patent No. US20020155110A1

; GENERAL INFORMATION:

; APPLICANT: GEMINI SCIENCE, INC.

; APPLICANT: Takahashi, No. US20020155110A1uaki

; APPLICANT: Mikayama, Toshifumi

; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAPA)

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE

; FILE REFERENCE: 021286/0278719

; CURRENT APPLICATION NUMBER: US/09/811,367B

; CURRENT FILING DATE: 2002-03-12

; PRIOR APPLICATION NUMBER: 60/190,716

; PRIOR FILING DATE: 2000-03-17

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 5

; LENGTH: 188

; TYPE: PRT

; ORGANISM: Rattus norvegicus

; US-09-811-367B-5

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Best Local Similarity 100.0%; Pred. No. 2.7e-99;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
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; ORGANISM: Mus musculus
US-09-811-367B-3

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QY 181 WICEKVL 187
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; Sequence 98, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16

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; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/10/741,790
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
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; PRIOR FILING DATE: 2000-05-24
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; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-741-790-98

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QY 92 EKRDWNSLKFADKADKSHLITFPDQGNVLFQEVVGEDFYWIGL---RDIDGRWEDGPA 148
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Db 65 SESSWNEISRDFCKGKSTLAIVNTPEKLFLODITDAEKYFGLIYHREKRWNNVSV 124
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 149 LSLISLNSVYQKGTTHRCGL-----HASSCEVALOWICEK 185
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 125 PNGVNTQNONFNCATI---GLTKTFDASCDISYRRIKCEK 162
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 5
US-09-766-511B-55
; Sequence 55, Application US/09766511B
; Publication No. US20030170621A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; APPLICANT: BARNES, Thomas S
; APPLICANT: KIRST, Susan J
; APPLICANT: MYERS, Paul S
; APPLICANT: WRIGHTON, Nicholas
; APPLICANT: GOODEARL, Andrew
; APPLICANT: HOLTZMAN, Douglas A
; APPLICANT: KHODADOUST, Mehran M
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-65
; CURRENT APPLICATION NUMBER: US/09/766,511B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/345,680
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; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-766-511B-55

Query Match      16.2%; Score 167.5; DB 10; Length 161;
Best Local Similarity 28.7%; Pred. No. 3.2e-09;
Matches 43; Conservative 21; Mismatches 71; Indels 15; Gaps 4;

QY 50 LMSLLLYQRTLCCGSKGFMCSQCRCPNLWMRNGSHCYVFSMEKRDWNSLKFADKADK 109
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 6 LSELHSHSLTCTFSEGTVPAGWCCPASWKFSGSSCYFISSEKYSKQNCVEMGAH 65
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 110 LITFPDQGNVLFQEVVGEDFYWIGLRDIDG---WRWEDGPALSIL-----SNSVV 159
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 66 LVVFNTAEQNFTVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPN 125
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 160 QKCGTI-----HRCGLHASSCEVALOWICE 184
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 126 EQCASIVFWKPTGWNVDVICETRRNSICE 155
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 6
US-09-764-870-310
; Sequence 310, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 310
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-764-870-310

Query Match      15.9%; Score 164.5; DB 9; Length 182;
Best Local Similarity 26.9%; Pred. No. 7.7e-09;
Matches 36; Conservative 22; Mismatches 59; Indels 17; Gaps 5;

QY 62 CGSKGFMCSQCRCPNLWMRNGSHCYVFSMEKRDWNSLKFADKADKSHLITFPDQGN 121
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 54 CASRS--ADQTVLCQSEWLKYQKCYWFSNEMKSWDSYVYCLERKSHLLIHDLEWAF 111
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 122 FQEVVGE-DFYWIGLRDID---GWRWEDGPALSIL-----SNSVQKCGTTHRCGL 170
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 112 IQNLRQLNVWIGLNTSLKMTWTWVDGSPIDSKIFFIKPAKENS---CAALESKI 167
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 171 HASSCEVALOWICE 184
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 168 FSETCSSVFKWICQ 181
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 7
US-10-125-540-310
; Sequence 310, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:40:40 ; Search time 14.5 Seconds
(without alignments)
669.357 Million cell updates/sec

Title: US-09-811-367b-5

Perfect score: 1036

Sequence: 1 MADNSYSLLELPAAARVQD.....GLHASCEVALQWICKVLP 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 303002

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgm2_6/ptodata/2/iaa/5A COMB.pep.*

2: /cgm2_6/ptodata/2/iaa/5B COMB.pep.*

3: /cgm2_6/ptodata/2/iaa/6A COMB.pep.*

4: /cgm2_6/ptodata/2/iaa/6B COMB.pep.*

5: /cgm2_6/ptodata/2/iaa/PCTUS COMB.pep.*

6: /cgm2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1036	100.0	188	3	US-08-722-126A-5
2	1036	100.0	188	5	PCT-US95-04258-5
3	651	62.8	114	3	US-08-722-126A-6
4	651	62.8	114	5	PCT-US95-04258-6
5	273	26.4	76	4	US-09-531-056A-23
6	166.5	16.1	115	3	US-08-722-126A-8
7	166.5	16.1	115	5	PCT-US95-04258-8
8	158.5	15.3	167	3	US-08-772-440-21
9	155	15.0	179	1	US-08-690-095-9
10	155	15.0	179	2	US-08-650-578-2
11	155	15.0	179	2	US-08-688-342-3
12	155	15.0	179	2	US-09-113-788-3
13	155	15.0	179	3	US-09-113-789-9
14	153	14.8	122	3	US-08-722-126A-9
15	153	14.8	122	5	PCT-US95-04258-9
16	153	14.8	126	3	US-08-772-440-10
17	153	14.8	134	3	US-08-543-246B-20
18	153	14.8	176	3	US-08-772-440-8
19	153	14.8	180	3	US-08-772-440-31
20	153	14.8	187	4	US-09-127-946-12
21	149.5	14.4	168	3	US-08-772-440-17
22	148	14.3	173	4	US-09-531-056A-4
23	147.5	14.2	79	4	US-09-531-056A-19
24	145.5	14.0	129	3	US-08-722-126A-10
25	145.5	14.0	129	5	PCT-US95-04258-10
26	142	13.7	175	3	US-08-772-440-15
27	140	13.5	78	4	US-09-531-056A-18

Sequence 16, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 23, Appl
Sequence 27, Appl
Sequence 14, Appl
Sequence 22, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 21, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-722-126A-5
Query Match 100.0%; Score 1036; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.3e-105;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVODDSRWKVKAVLHRCPCVSYLWVALGLLTVILMSLLYQRTL 60
DB 1 MADNSIYSTLELPAAPRVODDSRWKVKAVLHRCPCVSYLWVALGLLTVILMSLLYQRTL 60

QY 61 CCGSKGFMCSQCSRCPNLWMRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVN 120
DB 61 CCGSKGFMCSQCSRCPNLWMRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVN 120

QY 121 LFOEYVGDFFYIGLRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGDFFYIGLRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQ 180

QY 181 WICEKVLP 188
DB 181 WICEKVLP 188

RESULT 2

PCT-US95-04258-5

; Sequence 5, Application PC/TUS9504258

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL

; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04258

; FILING DATE: 06-APR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 109257

; FILING DATE: 08-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: PECHT-1 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 188 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-04258-5

Query Match 100.0%; Score 1036; DB 5; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.3e-105;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVODDSRWKVKAVLHRCPCVSYLWVALGLLTVILMSLLYQRTL 60
DB 1 MADNSIYSTLELPAAPRVODDSRWKVKAVLHRCPCVSYLWVALGLLTVILMSLLYQRTL 60

QY 61 CCGSKGFMCSQCSRCPNLWMRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVN 120
DB 61 CCGSKGFMCSQCSRCPNLWMRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVN 120

QY 121 LFOEYVGDFFYIGLRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGDFFYIGLRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQ 180

QY 181 WICEKVLP 188
DB 181 WICEKVLP 188

RESULT 3

US-08-722-126A-6

; Sequence 6, Application US/08722126A

; Patent No. 6034227

; GENERAL INFORMATION:

; APPLICANT: PECHT, Israel

; APPLICANT: GUTHMANN, Marcelo D.

; APPLICANT: TAL, Michael

; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL

; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

; STREET: 419 Seventh Street N.W., Ste. 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/722,126A

; FILING DATE: 08-OCT-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04258

; FILING DATE: 06-APR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 109257

; FILING DATE: 08-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: PECHT-1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 628-5197

; TELEFAX: (202) 737-3528

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 114 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-722-126A-6

Query Match 62.8%; Score 651; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.7e-64;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 CPNLWMRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVNLFQEVYVGDFFYWG 134
DB 1 CPNLWMRNGSHCYFFSMKRDWNSLKFCDKAGSHLLTFPDNQGVNLFQEVYVGDFFYWG 60

QY 135 LRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQWICEKVLP 188
DB 61 LRDIDGWRWEDGPALSLILNSVVKCGTTHRCGLHASSCEVALQWICEKVLP 114

RESULT 4

PCT-US95-04258-6

```
; Sequence 6, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04258-6

Query Match 62.8%; Score 651; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.7e-64;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 CPNLMWRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFPDNQGVLNLFQEVYVGEDFYWIG 134
Db 1 CPNLMWRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFPDNQGVLNLFQEVYVGEDFYWIG 60

Qy 135 LRIDGWRWEDGPALSLSLNSVVKCGTTHRCGLHASSCEVALQWICEKVP 188
Db 61 LRIDGWRWEDGPALSLSLNSVVKCGTTHRCGLHASSCEVALQWICEKVP 114

RESULT 5
US-09-531-056A-23
; Sequence 23, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-23
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Query Match 26.4%; Score 273; DB 4; Length 76;
Best Local Similarity 59.7%; Pred. No. 1.4e-22;
Matches 43; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy 75 CPNLMWRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFPDNQGVLNLFQEVYVGEDFYWIG 134
Db 3 CPDWMKYGKHCYFYSVEEKDWNSSLEFLCLARDSHLLVITDQEMSLQLQVFLSEAFQWIG 62

Qy 135 LRIDGWRWEDG 146
Db 63 LRNMSCWRWEDG 74

RESULT 6
US-08-722-126A-8
; Sequence 8, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-8

Query Match 16.1%; Score 166.5; DB 3; Length 115;
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 31; Conservative 22; Mismatches 57; Indels 3; Gaps 2;

Qy 75 CPNLMWRNGSHCYFYSMEKRDWNSLKFCDKSGSHLLTFPDNQGVLNLFQEVYVGEDFYWIG 134
Db 1 CSEDWVGQKCYFISTVKRSWTSQAACSEHGATLAVIDSEKDNFLKRYAGEEHVWG 60

Qy 135 LRIDG--WRWEDGPALSLSLNSVVKCGTTHRCGLHASSCEVALQWICEK 185
Db 61 LKKEPGHPKWSNGKEFN-NWFNVTGSDKCVFLKNTVSSMECEKNLYWICK 112
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RESULT 7

PCT-US95-04258-8
; Sequence 8, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY, Roger L.
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECTH=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04258-8

Query Match 16.1%; Score 166.5; DB 5; Length 115;
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 31; Conservative 22; Mismatches 57; Indels 3; Gaps 2;
QY 75 CPNLMWRNGSHCYFFSMKRDWNSLKFCAKDGSHLLTFPDNQGVNLFQYVGEDFYWIG 134
Db 1 CSEDWVGQKCYFISTVKRSWTSQAQACSEHGATLAVIDSEKDNFLKRYAGREEHWVG 60
QY 135 LRDIDG--WRWEDGPALSLSILNSVQKGTIHRGGLHASCEVALQWICEK 185
Db 61 LKKEGHPKWSNGKEFN--WNFNVTGSDKCVFLKXNTEVSSMECEKNLYWICNK 112

RESULT 8

US-08-772-440-21
; Sequence 21, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston

STATE: Texas
COUNTRY: USA
ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-21

Query Match 15.3%; Score 158.5; DB 3; Length 167;
Best Local Similarity 28.6%; Pred. No. 1.3e-09;
Matches 44; Conservative 23; Mismatches 66; Indels 21; Gaps 6;
QY 50 LMSLLLYQRTLCGSKGFMCSQ-----CSRCPNLMWRNGSHCYFFSMKRDWNSLKFCAK 105
Db 10 LYELHTYHSSLTCTFSEGTWSEKMWGC--CPNHWKSGSCYLSTKENFWSSTSQNCVQ 67
QY 106 KGSHLLTFPDNQGVNLFQYVGEDFYWIGLRDIDG---WRWEDGPALSLSIL-----S 155
Db 68 MGAHLVINTREAEQNFITQQLNESLSYFLGSLDPQGNKGKQWIDDTTFSQNVRFWHPHEP 127
QY 156 NSVQKCGTI-----HRCGLHASCEVALQWICE 184
Db 128 NLPEERCVSIVYWNPSKMGWMDVFCDSKHNSICE 161

RESULT 9

US-08-690-095-9
; Sequence 9, Application US/08690095
; Patent No. 5792648
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,095
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US


```
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 179 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 1098617
/
US-08-650-578-9
Query Match 15.0%; Score 155; DB 1; Length 179;
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;

Qy 24 WK-VKAVLHRCVSYLVMMVALGLLTVILMSLLYQRTLCGSKGFM--CSQCRCPCPNLWM 80
Db 9 WRLISGTLGIIICLS--LMATIGILLKNSFTKLSIEPAFTPGPNIELQKSDCCSCQEKWV 66
Qy 81 RNSGHCYFYSMEKRDWNSSLKFCADKSGSHLLTPDNQGVNLFQRYVGEDFYWIGL---RD 137
Db 67 GYRCNCYFISSEQKTNWESHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEE 124
Qy 138 IDGWRWEDGPALSILSILNSV--VOKCGTTHRCG-LHASSCEVALQWICEKVL 187
Db 125 HTAWLWENGSAISQYLFPSFETFTKNCIAYNPNGNALDESCDKNRYICKQQL 178

RESULT 10
US-08-650-578-2
Sequence 2, Application US/08650578
Patent No. 5811284
GENERAL INFORMATION:
APPLICANT: Chang, Chiwen
APPLICANT: Aramburu Beltran, Jose
APPLICANT: Lopez-Botet, Miguel
APPLICANT: Phillips Jr., Joseph H.
APPLICANT: Lanier, Lewis L.
TITLE OF INVENTION: Purified Mammalian NK Antigens and
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,578
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,339
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1098616
US-08-688-342-3
Query Match 15.0%; Score 155; DB 2; Length 179;
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;

Qy 24 WK-VKAVLHRCVSYLVMMVALGLLTVILMSLLYQRTLCGSKGFM--CSQCRCPCPNLWM 80
Db 9 WRLISGTLGIIICLS--LMATIGILLKNSFTKLSIEPAFTPGPNIELQKSDCCSCQEKWV 66
Qy 81 RNSGHCYFYSMEKRDWNSSLKFCADKSGSHLLTPDNQGVNLFQRYVGEDFYWIGL---RD 137
Db 67 GYRCNCYFISSEQKTNWESHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEE 124
Qy 138 IDGWRWEDGPALSILSILNSV--VOKCGTTHRCG-LHASSCEVALQWICEKVL 187
Db 125 HTAWLWENGSAISQYLFPSFETFTKNCIAYNPNGNALDESCDKNRYICKQQL 178

RESULT 11
US-08-688-342-3
Sequence 3, Application US/08688342
Patent No. 5871964
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1098616
US-08-688-342-3
Query Match 15.0%; Score 155; DB 2; Length 179;
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;

Qy 24 WK-VKAVLHRCVSYLVMMVALGLLTVILMSLLYQRTLCGSKGFM--CSQCRCPCPNLWM 80
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Db 9 WRLISGTLGIIICLS--LMATLGIILKNSFTKLSIEPAFTPGPNIELQKSDCCSCQEKWV 66
QY 81 RNSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGNLFQEVYVGDFYWIGL---RD 137
Db 67 GYRCNCYFISSEQKWTNESHLCASQKSSLLQNTDDELDFMSS--SQQFYWIGLSYSEE 124
QY 138 IDGWRWEDGPALSLSLNSV---VQKCGTHRCG-LHASSCEVALQWICEKVL 187
Db 125 HTAWLWENGSAISOYLFPSEFTFNKNCIAYPNNGNALDESDCKNRYICKQOL 178

RESULT 12
US-09-113-788-3
; Sequence 3, Application US/09113788
; Patent No. 5969104
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/688,342
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
US-09-113-788-3

Query Match 15.0%; Score 155; DB 2; Length 179;
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;
QY 24 WK-VKAVLHRCVSVLYMVALGLLTIVILMSLLVQRTLCCSGKGM--CSQCSRCPNLWM 80
Db 9 WRLISGTLGIIICLS--LMATLGIILKNSFTKLSIEPAFTPGPNIELQKSDCCSCQEKWV 66
QY 81 RNSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGNLFQEVYVGDFYWIGL---RD 137
Db 67 GYRCNCYFISSEQKWTNESHLCASQKSSLLQNTDDELDFMSS--SQQFYWIGLSYSEE 124
QY 138 IDGWRWEDGPALSLSLNSV---VQKCGTHRCG-LHASSCEVALQWICEKVL 187

Db 125 HTAWLWENGSAISOYLFPSEFTFNKNCIAYPNNGNALDESDCKNRYICKQOL 178

RESULT 13
US-09-113-789-9
; Sequence 9, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
US-09-113-789-9

Query Match 15.0%; Score 155; DB 3; Length 179;
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;
QY 24 WK-VKAVLHRCVSVLYMVALGLLTIVILMSLLVQRTLCCSGKGM--CSQCSRCPNLWM 80
Db 9 WRLISGTLGIIICLS--LMATLGIILKNSFTKLSIEPAFTPGPNIELQKSDCCSCQEKWV 66
QY 81 RNSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGNLFQEVYVGDFYWIGL---RD 137
Db 67 GYRCNCYFISSEQKWTNESHLCASQKSSLLQNTDDELDFMSS--SQQFYWIGLSYSEE 124
QY 138 IDGWRWEDGPALSLSLNSV---VQKCGTHRCG-LHASSCEVALQWICEKVL 187
Db 125 HTAWLWENGSAISOYLFPSEFTFNKNCIAYPNNGNALDESDCKNRYICKQOL 178

RESULT 14
US-08-722-126A-9
; Sequence 9, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:

```

; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-9
;
; Query Match 14.8%; Score 153; DB 3; Length 122;
; Best Local Similarity 27.9%; Pred. No. 3.5e-09;
; Matches 34; Conservative 22; Mismatches 56; Indels 10; Gaps 4;
;
Qy 75 CPNLWMRNGSHCYFYSMEKRDWNSLKFCDKAGSHLLTFPDNQGVNLFQEVVGEDF--YW 132
Db 1 CPQDWLSHRDKCFHVSQVSNTWEEGLVDCDGKATMLIQDEELRFLDLSIKEKNSFW 60
Qy 133 IGLR---DIDGWRWEDGPALS---LSILSNVVKCGTTHRCGLHASSCEVALQWICEK 185
Db 61 IGLRYTLPDNM-WKWINGSTLNSDLKITGTENDSCAAISGDKVTFESCNSDNRWICQK 119
Qy 186 VL 187
Db 120 EL 121

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; RESULT 15
; PCT-US95-04258-9
; Sequence 9, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington

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; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04258-9
;
; Query Match 14.8%; Score 153; DB 5; Length 122;
; Best Local Similarity 27.9%; Pred. No. 3.5e-09;
; Matches 34; Conservative 22; Mismatches 56; Indels 10; Gaps 4;
;
Qy 75 CPNLWMRNGSHCYFYSMEKRDWNSLKFCDKAGSHLLTFPDNQGVNLFQEVVGEDF--YW 132
Db 1 CPQDWLSHRDKCFHVSQVSNTWEEGLVDCDGKATMLIQDEELRFLDLSIKEKNSFW 60
Qy 133 IGLR---DIDGWRWEDGPALS---LSILSNVVKCGTTHRCGLHASSCEVALQWICEK 185
Db 61 IGLRYTLPDNM-WKWINGSTLNSDLKITGTENDSCAAISGDKVTFESCNSDNRWICQK 119
Qy 186 VL 187
Db 120 EL 121

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; Search completed: August 10, 2004, 16:45:20
; Job time : 14.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:11:32 ; Search time 32.7823 Seconds
(without alignments)
1819.059 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MTDSDVIYSMLPQTATQON.....GLQASCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1023	100.0	189	4	O43198
2	1007	98.4	189	4	O75613
3	994	97.2	195	4	O96E93
4	548.5	53.6	188	11	O88713
5	525.5	51.4	188	11	O64335
6	226	22.1	231	4	Q9NZS2
7	225	22.0	181	4	Q9NZS1
8	222	21.7	200	13	Q802S8
9	219.5	21.5	275	11	Q9D403
10	219	21.4	231	6	Q8MT05
11	210	20.5	227	11	O9WU32
12	210	20.5	231	11	O54872
13	205	20.0	200	6	Q8SPX1
14	201.5	19.7	231	6	Q9MZK3
15	201	19.6	225	4	Q12918
16	201	19.6	233	6	Q8MJH7

17	200	19.6	233	6	Q8MJH6	Q8mjh6 pongo pygma
18	199.5	19.5	207	11	Q8BHH6	Q8bhh6 mus musculus
19	199.5	19.5	231	6	Q9GK88	Q9gk88 macaca mula
20	199.5	19.5	269	11	Q9D676	Q9d676 mus musculus
21	199	19.5	196	11	Q8VI21	Q8vi21 mus musculus
22	199	19.5	233	6	Q8MJT0	Q8mjt0 pongo pygma
23	199	19.5	233	6	Q9MYM6	Q9nym6 pan troglod
24	197	19.3	232	11	O54709	O54709 mus musculus
25	196.5	19.2	246	6	Q9MZK2	Q9mzk2 macaca mula
26	196	19.2	211	11	Q91ZW5	Q91zw5 mus musculus
27	196	19.2	246	6	Q9MZK1	Q9mzk1 macaca mula
28	195.5	19.1	244	11	Q9Z202	Q9z202 mus musculus
29	195.5	19.1	278	6	Q9XTA8	Q9xta8 oryctolagus
30	194.5	19.0	178	11	Q91ZW9	Q91zw9 mus musculus
31	194	19.0	233	6	Q8MJH5	Q8mjh5 pongo pygma
32	193	18.9	233	6	Q8MJH8	Q8mjh8 pongo pygma
33	193	18.9	233	6	Q8MJH9	Q8mjh9 pongo pygma
34	193	18.9	257	13	Q90636	Q90636 gallus gall
35	193	18.9	270	6	P79391	P79391 bos taurus
36	192.5	18.8	208	11	Q91ZW7	Q91zw7 mus musculus
37	192.5	18.8	244	11	Q9WU31	Q9wu31 mus musculus
38	192	18.8	236	6	Q95L94	Q95l94 macaca mula
39	191.5	18.7	230	11	O54871	O54871 rattus norv
40	190	18.6	199	6	Q95MQ1	Q95mq1 bos taurus
41	190	18.6	227	11	Q61973	Q61973 mus musculus
42	190	18.6	233	6	Q8MJ11	Q8mj11 pongo pygma
43	189.5	18.5	179	6	Q8MJ13	Q8mj13 pongo pygma
44	189.5	18.5	179	6	Q8MHY8	Q8mhy8 pongo pygma
45	189	18.5	216	6	Q8MJH0	Q8mjh0 pongo pygma

ALIGNMENTS

RESULT 1

O43198 ID O43198 PRELIMINARY; PRT; 189 AA.
AC O43198;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Mast cell function-associated antigen.
GN MAF A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98438735; PubMed=9765598;
RA Lamers M.B., Lamont A.G., Williams D.H.;
RT "Human MAF A has alternatively spliced variants.";
RL Biochim. Biophys. Acta 1399:209-212(1998).
DR ENBL; AF034952; AAC34731.1; .
DR GO; GO:001621; C-integral to membrane; TAS.
DR GO; GO:0003793; F:defense/immunity protein activity; TAS.
DR GO; GO:0005530; F:lectin; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT. 1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 189 AA; 21079 MW; 15E042AD40B2B4F6 CRC64;

Query Match 100.0%; Score 1023; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 7, 4e-105;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDSDVIYSMLPQTATQANDYGPQOKSSSKPSCSLVAITGLLTAVLLSVLLYQWIL 60

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Db 1 MTDSVIYSMLPLPTATQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
QY 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
Db 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
QY 181 HGVCCKVRL 189
Db 181 HGVCCKVRL 189

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RESULT 2

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O75613 PRELIMINARY; PRT; 189 AA.
AC O75613;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ITIM-containing receptor MAFA-L.
GN MAFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Butcher S., Arney K.L., Cook G.P.;
RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene
RT complex and expressed by basophils and NK cells.";
RL Eur. J. Immunol. 28:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 'Sl', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
DR EMBL; AF081675; AAC32200.1; -.
DR EMBL; AF097358; RAD03719.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

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Query Match 98.4%; Score 1007; DB 4; Length 189;
Best Local Similarity 98.4%; Pred. No. 4.3e-103;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDSVIYSMLPLPTATQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYSMLPLPTATQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
QY 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
Db 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
QY 181 HGVCCKVRL 189
Db 181 HGVCCKVRL 189

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RESULT 3

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Q96E93 PRELIMINARY; PRT; 195 AA.
AC Q96E93;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Similar to killer cell lectin-like receptor subfamily G, member 1.
DE 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Strausberg R.;
RL EMBL; BC012621; AAHL2621.1; -.
DR GenBank; HGNC:6380; KLRG1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 195 AA; 21831 MW; 178EE98E08EBC473 CRC64;

Query Match 97.2%; Score 994; DB 4; Length 195;
Best Local Similarity 98.4%; Pred. No. 1.2e-101;
Matches 183; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDSVIYSMLPLPTATQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYSMLPLPTATQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
Db 61 CQGSNYSTCASCPCPDRAWKMGHCHYFVSVEEKDWNSSLEFCLARDSHLLVITDNQMS 120
QY 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
Db 121 LLOVFLSEAFWIGLIRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASCEVPL 180
QY 181 HGVCCK 186
Db 181 HGVCCK 186

RESULT 4
O88713 PRELIMINARY; PRT; 188 AA.
AC O88713;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-AUG-1999 (TREMELrel. 11, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).
GN KLRG1 OR MAFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99077194; PubMed=9862378;
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 'Sl', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
RN [2]

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RP SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvevTACfBr; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=1120622;
RA Voehlinger D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor G1 gene (KLRF1), the mouse homologue
RT of MAFK.";
RL Immunogenetics 52:206-211(2001).
DR EMBL; AF097357; AAD03718.1; -.
DR EMBL; AJ010751; CAA09342.1; -.
DR EMBL; AF317727; AAK40082.1; -.
DR MGD; MGI:1355294; Klrg1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR SMART; SM00034; Lectin_c; 1.
DR PROSITE; PSS00041; C_TYPE_LECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match 53.68; Score 548.5; DB 11; Length 188;
Best Local Similarity 55.68; Pred. No. 2.1e-52;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDVSYMLELPTATQAQNDYGPQQKSSSKPSCSLVAITLGLLFAVLLSVLLYQWIL 60
Db 1 MADSSYSTLELPEAPQVQDESQKLVKAVLHRLSFPANVALLGLTVILMSLLMQRIIL 60

QY 61 CQGSNTSTCASCPDRMKYGNHCYFVSVEKDNSSLEFCLARDSHLLVITDQEMS 120
Db 61 CCGSKDSTCHSPCLPILTRNGSHCYFYSMEKRDWNSLKFCADKSHLLTFPDNGVK 120

QY 121 LLQVFLSEAFQWIGLRNNGWRWEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL 180
Db 121 LFGEYLGQDFYWTGLRNDIGRWEGGPAALS-LRLTNSLQRCGAIRNGLOASSCEVAL 179

QY 181 HGVCCKV 187
Db 180 QWICKV 186

RESULT 5
Q64335 PRELIMINARY; PRT; 188 AA.
AC Q64335;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE MAFK protein.
DE MAFK.
GN MAFK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=Testis;
RA Bocke Jr P., Guthmann M.D., Pecht I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016176; PubMed=7568140;
RA Guthmann M.D., Tal M., Pecht I.;
RT "A secretion inhibitory signal transduction molecule on mast cells is
RT another C-type lectin.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL; X97191; CAA65829.1; -.

SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvevTACfBr; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=1120622;
RA Voehlinger D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor G1 gene (KLRF1), the mouse homologue
RT of MAFK.";
RL Immunogenetics 52:206-211(2001).
DR EMBL; AF097357; AAD03718.1; -.
DR EMBL; AJ010751; CAA09342.1; -.
DR EMBL; AF317727; AAK40082.1; -.
DR MGD; MGI:1355294; Klrg1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR SMART; SM00034; Lectin_c; 1.
DR PROSITE; PSS00041; C_TYPE_LECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match 51.48; Score 525.5; DB 11; Length 188;
Best Local Similarity 53.58; Pred. No. 7.2e-50;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDVSYMLELPTATQAQNDYGPQQKSSSKPSCSLVAITLGLLFAVLLSVLLYQWIL 60
Db 1 MADNSYSTLELPAAPRVQDDSRWKVAVLHRCVSLVWVALLGLTVILMSLLYQRTL 60

QY 61 CQGSNTSTCASCPDRMKYGNHCYFVSVEEKNSSLEFCLARDSHLLVITDQEMS 120
Db 61 CCGSKGFMCSQCSCPCNLMWRNGSHCYFYSMEKRDWNSLKFCADKSHLLTFPDNGVN 120

QY 121 LLQVFLSEAFQWIGLRNNGWRWEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL 180
Db 121 LFGEYVGDFYWTGLRIDGWRWEDGPAALS-ILNSVYVQKGTIHRCLGHASSCEVAL 179

QY 181 HGVCCKV 187
Db 180 QWICKV 186

RESULT 6
Q9NZS2 PRELIMINARY; PRT; 231 AA.
AC Q9NZS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lectin-like receptor F1 (Activating coreceptor NKp80).
GN KLRF1 OR ML/KLRF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KLRF1, a novel member of the killer cell lectin-like receptor
RT gene family; molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=Lymphoid;
RX MEDLINE=21150889; PubMed=11265639;
RA Vitale M., Falco M., Castriconi R., Parolini S., Zambello R.,
RA Semenzato G., Biassoni R., Bottino C., Moretta L., Moretta A.;
RT "Identification of NKp80, a novel triggering molecule expressed by
RT human natural killer cells.";
RL Eur. J. Immunol. 31:233-242(2001).
DR EMBL; AF175206; AAF37804.1; -.
DR EMBL; AJ305370; CAC29425.1; -.
DR Genew; HGNC:13342; KLRF1.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; Lectin_C.

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DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 231 AA; 26562 MW; A2F7BE6D4341AFDE CRC64;

Query Match
Best Local Similarity 22.1%; Score 226; DB 4; Length 231;
Matches 58; Conservative 27; Mismatches 53; Indels 48; Gaps 8;

Qy 44 GLTAVLLSVLLY--QWTL--CQG-----SNYSTCASCPS 74
Db 49 GILTLTSLILLVSGVLLKCKGSCSNATQYEDTGLKVNNGRRNRISNKLDCASRSA 108
Qy 75 -----CPDRWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSLLOVFLSEA 129
Db 109 DQTVLCQSEWLKQCKYCFWFSNEMKWSDSVYVCLERKSHLLIITHDQLEMAFIQKNLRQL 168
Qy 130 -FCWIGLRNNS---GWRWEDGSLNFRISNSFVQ-----TCGAINKGLQASSCEVP 179
Db 169 NYVIGLNTSLKMTWTWVDGSPID----SKIFIKGPAKENSAAIKESKIFSETCSSV 224
Qy 180 LHGVCK 185
Db 225 FKWICQ 230

RESULT 7
ID Q9NZS1 PRELIMINARY; PRT; 181 AA.
AC Q9NZS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lectin-like receptor Fl, splice variant 1 KLRFL-sl.
GN KLRFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kuchelapati R.,
RA Fernandez-Ruiz E.;
RT "Human KLRFL, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
DR EMBL; AF175207; AAF37805.1; -.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CAE1E551 CRC64;

Query Match
Best Local Similarity 22.0%; Score 225; DB 4; Length 181;
Matches 51; Conservative 26; Mismatches 45; Indels 30; Gaps 6;

Qy 44 GLTAVLLSVLLYQWILCQGSNYSCASCPCPDWMMKYGNHCYFVSVEEKDWNSSLEFC 103
Db 49 GILTLTSLILL--VLCQ-----SEWLKQCKYCFWFSNEMKWSDSVYVC 92
Qy 104 LARDSHLLVITDQEMSLLOVFLSEA-FCWIGLRNNS---GWRWEDGSLNFRISNSF 159
Db 93 LERKSHLLIITHDQLEMAFIQKNLRQLNYVWIGLNTSLKMTWTWVDGSPID----SKIFF 148
Qy 160 VQ-----TCGAINKGLQASSCEVPLHGVC 195
Db 160 VQ-----TCGAINKGLQASSCEVPLHGVC 195

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Db 149 IKGPAKENSAAIKESKIFSETCSSVFKWICQ 180

RESULT 8
ID Q802S8 PRELIMINARY; PRT; 200 AA.
AC Q802S8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-type lectin.
GN Y-LEC2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Rogers S., Shaw I., Ross N., Nair V., Rothwell L., Kaufman J.,
RA Kaiser P.;
RT "Analysis of part of the chicken Rfp-Y region reveals two novel lectin
RT genes, a truncated class II beta-chain gene, and a large CR1 repeat.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277927; CAD61336.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR002353; Antifreeze1.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZE1I.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 200 AA; 22573 MW; 23AA950D113349B8 CRC64;

Query Match
Best Local Similarity 21.7%; Score 222; DB 13; Length 200;
Matches 53; Conservative 31; Mismatches 67; Indels 42; Gaps 7;

Qy 23 GPQOKS-----SSSKPSCSC-----LVAITGLLTAVLLSVLLYQWILCQGSNY 66
Db 7 GDQGETFSEHQATEPRSWCHGARRSRVQLIAVCAALGALILVLVI-----S 56
Qy 67 STCASC-----SOPDRMMKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQ 117
Db 57 TVCRQVPPPPDFFAHACPNWVGFGQCKYFSEKENDWNSSREHCNAHGLATIGSAE 116
Qy 118 EMSLLQVFLSEAFWCWIGL---RNNSGWRWEDGSLNFRISNSFVQTCGAINKGLQ 173
Db 117 EMDFMRFQGPANCWIGLHREEDAQWTSQDTFTNWFELRGSG---RCAYLNGDRISS 173
Qy 174 SSCVPLHGVCCK 186
Db 174 SLCHLKHVWCSR 186

RESULT 9
ID Q9D403 PRELIMINARY; PRT; 275 AA.
AC Q9D403;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 4933425B1erik protein.
GN 4933425B1ERIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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Db      62 KGFPSPPEKLIAGTLGLICFLVLIIVAVVVITTVATPYINVTYSSAQCPCHPKEMISYSHN 121
Qy      86 CYFESVERKWNSSLEFCLARDSHLLVITDQEMSLLOVFLSEAFPCWIG-IRNNSG--WR 142
Db      122 CYFTIGMERKSWNDLSVSCISKNCSLLYIDSEEQDFLOSL--SLISWTGILRKGRGPWV 179
Qy      143 WEDSGPLNFSIRSSNSFVQ-----TCCAINKNGIQAASSCEVPLHGVCK 185
Db      180 WKEDS-----IFPKIAEILHDECNCAMMSASGLTADNCTYTHPYLCK 222

RESULT 12
Q54872
ID      054872 PRELIMINARY; PRT; 231 AA.
AC      054872
DT      01-JUN-1998 (TREMBLrel. 06, Created)
DT      01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Natural killer cell protein group 2-A (Fragment).
GN      NK2A.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=F344;
RX      MEDLINE=98180346; PubMed=9521051;
RA      Berg S.F., Dissen E., Westgaard I.H., Fossum S.;
RT      "Molecular characterization of two genes in the rat homologous to
RT      human NK2A.";
RL      Eur. J. Immunol. 28:444-450(1998).
DR      EMBL; AF021350; AAC40050.1; -.
DR      GO; GO:0005529; F:sugar binding; IEA.
DR      InterPro; IPR002353; AntifreezeII.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; lectin_c; 1.
DR      PRINTS; PR00356; ANTIFREEZEII.
DR      SMART; SM00034; CLECT; 1.
DR      PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
FT      NON TER 1
SQ      SEQUENCE 231 AA; 26335 MW; FF2AB6D33EF2CE99 CRC64;

Query Match 20.5%; Score 210; DB 11; Length 231;
Best Local Similarity 29.0%; Pred. No. 6.9e-15;
Matches 54; Conservative 25; Mismatches 81; Indels 26; Gaps 5;

Qy      24 PQKSSSKPKSC-----LVAITLGLTAVLLSVLL-----YQWILCOGSNY 66
Db      43 PSQEQTRICRDCCKGFFSPPEKLIAGTLGLFISFLVIAVVVITTVATPYTETKAQINS 102
Qy      67 ST-----CASCPCDPRWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSL 122
Db      103 MTRTYQARFCTRCDDWISYSHNCYIISVERKSWNDGLTSCIKNSCLLHDSBEQAPL 162
Qy      123 QVFLSEAFPCWIGIRNNS---GWRWEDGSLNFSRISNSFVTCGAINKNGIQAASSCEVP 179
Db      163 QSF--SLVSWTGFFPKRSQRPVWENGSTFKPIITMLHDEYINCIMMSTSGLTAEHCITLL 220

Qy      180 LHGVCK 185
Db      221 HPYVCK 226

RESULT 13
Q8SPX1
ID      Q8SPX1 PRELIMINARY; PRT; 200 AA.
AC      Q8SPX1
DT      01-JUN-2002 (TREMBLrel. 21, Created)
DT      01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Type II membrane protein CD69.
OS      Sus scrofa (Pig).

```

```

OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yim D., Sotiriadis J., Kim K.-S., Shin S.-C., Jie H.-B.,
RA      Rothschild M.F., Kim Y.B.;
RT      "Molecular cloning, expression pattern, and chromosomal mapping of pig
RT      CD69.";
RT      Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL      EMBL; AF484233; AAL91546.1; -.
DR      GO; GO:0005529; F:sugar binding; IEA.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; lectin_c; 1.
DR      SMART; SM00034; CLECT; 1.
DR      PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ      SEQUENCE 200 AA; 22257 MW; C55E8767E163A57C CRC64;

Query Match 20.0%; Score 205; DB 6; Length 200;
Best Local Similarity 29.6%; Pred. No. 2.1e-14;
Matches 56; Conservative 27; Mismatches 84; Indels 22; Gaps 9;

Qy      13 PTAQAQNDYCP-----QKSSSKP-SCSC--LVAITLGLTAVLLSVLLQWILCOGSN 65
Db      16 PNRGQPSNATGPHFATHHEGSLQVPIPCAVVNVVITVLIITLITALSQVYN--CPGOY 72
Qy      66 YSTCAS---CPSCDPRWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOE-MSL 121
Db      73 VPSVPSNMHVSCPDWDWIGYQTKYFISKYKNWTLAQSFCKKHGATLALLESKEDMVF 132
Qy      122 LQVFLSEAFPCWIGIRNNSG--WRWEDGSLN--FSRISNSFVTCGAINKNGIQAASSCE 177
Db      133 LKHVGRAEHWIGLKNEDGQTKWKSNGKEFNWPKLTGS---KNCPLNSTEVSMECE 188
Qy      178 VPLHGVCK 186
Db      189 KNLHWICK 197

RESULT 14
Q9MZK3
ID      Q9MZK3 PRELIMINARY; PRT; 231 AA.
AC      Q9MZK3
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      NK2-C.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC      Cercopithecinæ; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20322487; PubMed=10866118;
RA      LaBonte M.L., Levy D.B., Letvin N.L.;
RT      "Characterization of rhesus monkey CD94/NKG2 family members and
RT      identification of novel transmembrane-deleted forms of NK2-A, B, C,
RT      and D.";
RL      Immunogenetics 51:496-499(2000).
DR      EMBL; AF190937; AAF74533.1; -.
DR      HSSP; P22897; LEGS.
DR      GO; GO:0005529; F:sugar binding; IEA.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; lectin_c; 1.
DR      SMART; SM00034; CLECT; 1.
DR      PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ      SEQUENCE 231 AA; 26107 MW; COD307ABE0262DBD CRC64;

Query Match 19.7%; Score 201.5; DB 6; Length 231;
Best Local Similarity 29.8%; Pred. No. 6e-14;
Matches 59; Conservative 30; Mismatches 92; Indels 17; Gaps 7;

```

```
QY 2 TDSVIYSMLELPTAQAONDYGPQ--KSSSSKPSCLVAITLGLTAVLLSVLLYQWI 59
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
34 TEQEIP-QVELNLQPNVNHQGDQIYDCQGLLPPPEKLTAEVLGIICIVIMATVLTVV 92
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 LC---QGSNYS-----TCASCPSPDRWMKYGNHCYFVSVEEKDWNSSLEFCLARDSHL 110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
93 LIPPEQSSNLSNTRTKVRHCGHCPPEWITYNSCYIIGKERTWAEISLLACTSKNSSL 152
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 LVITDQEMSLLOVFLSEAFWIGL-RNNSGWRWEDGSPINFSRISNS--FVQTGCAGIN 167
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
153 LSIIDNEEMKFLTAILPSS--WIGVFNSSHPHFWVTINGLTFKHEIKNSDNASHNCAMLH 210
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 168 KNGLOASSCEVPLHGVCCK 185
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
211 ARGKSNQCESTVIYHCK 228
```

RESULT 15

```
Q12918
ID Q12918 PRELIMINARY; PRT; 225 AA.
AC Q12918;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE HNR-Pla protein.
GN HNR-Pla.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94358407; PubMed=8077657;
RA Lanier L.L., Chang C., Phillips J.H.;
RT "Human NKR-P1A: A disulfide-linked homodimer of the C-type lectin
RT superfamily expressed by a subset of NK and T lymphocytes.";
RL J. Immunol. 153:2417-2428(1994).
DR EMBL; U11276; AAA21605.1; -.
DR PIR; I38700; I38700.
DR HSP; P05140; ZAFP.
DR Gene; HGNC:6373; KLRB1.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005530; F:lectin; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 225 AA; 25415 MW; 01BFA925445B83B0 CRC64;
```

```
Query Match 19.6%; Score 201; DB 4; Length 225;
Best Local Similarity 26.0%; Pred. No. 6.6e-14;
Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTSVIYSMLELPTAQAONDYGPQKSSSKP-----SCSCLVAITLG 44
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MDQQAIFYAELNLT-----DSGPSSSPSLPRDVCQSPFHQFALKLSCAGIILLVL- 53
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 45 LLTAVLLSVLLYQWILCOGSNYSTCA-----SCPSPDRWMKYGNHCYFVS 90
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
54 VTGLSVST-----SLQKSIKCSVDIQQRNKTTFPGLLNCPYWOQLREKCLLFS 109
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 91 VEKDMNSSLFCLARDSHLITDQEMSLLOVFLSE--AFCWIGLR--NNSGWRWED 145
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
110 HTVNPWNNSLADCSKESLLLRDKDELHTQNLIRDKAILFWIGLNFSLSEKNWKNIN 169
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 146 GSPINFS--RISNSFVQTGCAGINKGLQASSCEVPLHGVCCK 186
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
170 GSFINSNDLIRDAKENSICISISQTSVSYGCGSTEIRWICQK 212
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Search completed: August 10, 2004, 16:18:48
Job time : 33.7823 secs

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